STIC-Biotech/ChemL	ib 174760
From: Sent: To: Subject:	Ramirez, Delia Tuesday, December 20, 2005 4:43 PM STIC-Biotech/ChemLib 10/049,750
Hi,	
I would like to request the fo	ollowing search:
1. a standard search of SE	Q ID NO: 11, 13 and 14 in the protein databases (commercial & interference)
Thank you very much,	
Delia M. Ramirez, Ph.D. Patent Examiner Recombinant Enzymes-Art Unit 1 USPTO 400 Dulany Street, Remsen Bldg Alexandria, VA 22314 (571) 272-0938 delia.ramirez@uspto.gov	

\*\*\*\*\*\*\*\*
Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search
NA#\_\_\_\_\_AA#:\_
S/L:\_\_\_Oligomer:\_\_\_
Encode/Transl:\_
Structure #:\_\_\_\_Text:\_
Inventor:\_\_\_\_Litigation:\_\_\_

Vendors and cost where applicable STN:

DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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                    Abo83136

Abb554213

Adc81814

Adc818171

Adv17572

Adm18771

Adm24710

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a deoxyribokinase enzyme
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ADN2 50 77
ADN2 50 77
ADN3 513
ABP5 5421
ADO8 3136
AAB73 533
AAM3 87175 72
AM3 20 3117
ADN2 21317
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAB67588 standard; protein; 306 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-1999; 99EP-00116425.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ihlenfeldt H,
 Tischer W, Ihlenfeldt
Marliere P, Pochet S;
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 Salmonella typhi.
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  Command line parameters:

-MODEL=frame+ in 2p. model - DEV=xlp
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-Gequary.fasta_1/1742
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-Geneseq -GFMT=fastan - SUFFIX=n2p.rag - MINNATCH=0.1 - LOOPCH=0 - LOOPEXT=0
-UNITS=bits -START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-UNITS=bits -START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-UNITS=bits -START=1 - END=-1 - MATRIX=100 - TRANS=human40.cdi - LIST=45
-UNTRAT=ptc - NORM=ext - HEAPSIZE=500 - MINISH=0 - MAXISH=200000000
-USER=USI0049750 @CGN 1 1 476 @runa + 23122005 113551 6285 - NCPI=6 - ICPU=3
-NO WMAP - LARGEQUERY - NEG SCORES=0 - THREAD=1 - XGAPOP=10 - LONGLOG
-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREAD=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
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Ad822364 Bacterial
Ad855248 Bacterial
Ad85578 Bacterial
Ad85578 Pacterial
Ad857378 Bacterial
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            GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                  protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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                                                                                       The present sequence represents a decoxyribokinase enzyme. This enzyme is involved in the biosynthesis of decoxyribonucleosides, and is used in the method of the invention. The specification describes a method for the invitro enzymatic synthesis of decoxyribonucleosides. The method comprises reacting decoxyribose 1-phosphate and anucleobase to form a decoxyribonucleoside and an inorganic phosphate. Enzymes which may be used in the method of the invention include thymidine phosphorylase, purine nucleoside phosphorylase, phosphorpencose mutase, phosphorpencose aldolase, fructose 1,6-diphosphate aldolase, decoxyribokinase, and nucleoside 2-
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                       ymatic synthesis of deoxyribonucleosides comprises reacting 1-phosphate and a nucleobase to form a deoxyribonucleoside
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                        In vitro enzymatic synthesis of
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                                               and an inorganic phosphate.
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  N-PSDB; AAF55444
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The invention relates to a library of DNA fragments of Escherichia colistrains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and encoded proteins (ABB52549-ABB52994-ABB53994) of nature B2/D4A. The polynucleotides have potential antinflammatory, antibacterial and immunosuppressive activity as part of pharmaceutical compositions used to treat, palliate or prevent extra-intestinal E. colinflationis. The polypeptides are useful for determining the phylogenic group of a given E. coli strain. These polypeptides can detect and treat an undesired development of E. coli, particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicaemia, pyelonephritis and meningitis this is particularly advantageous as bacterial resistence is increasing with the more frequent use of broad spectrum antibiotics
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                                                      TTCAGCGTCACCGGGAAAGGCACCCCAATCCTCTTATCCAAGCATTGAGCAATTTAATGAG
                                                                                                                                                            AGAGTGAACGCTGTTGATACCAGCGGCGCGGCGATGCCTTTATCGGCTGTTTCGCGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli; B2/D+A-; antiinflammatory; antibacterial; immunosuppressive; extra-intestinal infection; phylogeny; meningitis; systemic infection; non-diarrhoeal infection; septicaemia; pyelonephritis; antibiotic resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Proteus mirabilis polypeptides and polynucleotides, useful reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or biocontrol agents for plants.
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               301 PheLeuThrLeuAsnGlu
                                                                                                                                                                                                                         Bacterial polypeptide #1605
                                                                                                                                                                                   (first entry)
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                     Proteus mirabilis.
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2394
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                       7.13e-163
1519.00
98.69%
96.08%
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Best Local Similarity:
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                   Sequence 306
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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                               21-FEB-2002; 2002US-0360039P.
                                                                                                                  20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                 Hinkle GJ, Slater
bacterial polypeptide.
                                                                                                                                                                                      HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S.
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                                                         US2003233675-A1
                                                                                      18-DEC-2003.
                             Bacteria.
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                                                                                                                                                                                                                                                   361 ATCGATCGCGCGCGCAAGATTTAAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTT 420
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                                                                                       66 GlyAspAspIlePheAlaAspAsnThrIleMetAsnLeuGluSerTyrGly1leAsnThr
                                                                                                                                                                                                                                                                   206 GlulleArgGluAlaAlaTyrPheLeuLeuGluLysGlyPheLysAsnIlelleValThr
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                                                                                                                                                                                                          TTTGTACCTAATGAAACCGAGCTGGAAATATTAACCGGTATGCCAGTGGATACCTATGAC
                              46 AlaAsnGlnAlaValAlaAlaAlaAlaLysLeuAsnSerLysValMetMetLeuThrLysVal
                                                                        GGCGACGATATTTTTGCCGACAACACCATTCGTAATCTTGGAATCCTGGGGGGATCAATACG
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant construct and growing the transforming a plant with the recombinant DNA construct and growing the transforming a plant with the recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with increased resistance to herbicides, extreme osmocia conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of protein yield and/or phosphorus use and/or uptake, by modification of protein yield and/or providing improved plant growth and development under at least one stress conduction. This sequence represents a bacterial polypeptide used in the printed specification but was obtained in electronic forms of form part of the printed specification but was obtained in electronic forms.
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Mismatches:
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Matches:
Claim 1; SEQ ID NO 14829; 122pp; English.
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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                    20-FEB-2003; 2003US-00369493
                                                           21-FEB-2002; 2002US-0360039P
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CAGGCCGTGCCGCCTAAGCTCAATTCAAAAGTATTGATGTTGACCAAAGTGGGCGAC
                                                 GATATTTTGCCGACAACACCATTCGTAATCTCGAATCCTGGGGGATCAATACGACGTAT
                                                               AspvalPheAlaAspAsnThrIleArgAsnLeuAlaSerPheGlyValAspThrArgHis
                                                                                                 GTAGAAAAAGTACCGTGTACCAGCAGCGGCGTAGCGCCGATTTTCGTCAACGCCAACTCC
                                                                                                                CGCGCGCGCAAGATTTAAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTTCAGCTT
                                                                                                                                                                                                                                                                                                                                                                   607 CGCGCAGCGCCACGTTCGCTGGTAGATAAAGGGCTGAACAATATTATTGTCACCATGGGC
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              GAAACGGTTTATCACGCAATAGAATTTGGCAAGAAACACGGGATTGAAGTGTTATTAAAC
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypoptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant comprising an improved property comprises transforming a plant with the recombinant DNA construct and growing the transforming a plant with the compliant DNA construct is useful for improving plants with the recombinant DNA construct is useful for improving plants with improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme osmotic conditions apthogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, nitrogen or providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress providing improved plant growth and development under at least one stress condition. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form the form tells and to the sequence the form the printed specification but was obtained in electronic forms.
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64 AspValPheAlaAspAsnThrIleArgAsnLeuAlaSerPheGlyValAspThrArgHis 83
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                                  GTAGAAAAAGTACCGTGTACCAGCAGCGGCGTAGCGCCGATTTTCGTCAACGCCAACTCC
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224 AlaArgGlyAlaArgMetIleThrSerAspGluIleValAsnIleGluProValLysVal
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The inventional in a plant cell, where the promoter compirator or promoter functional in a plant cell, where the promoter compiration of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant comprising the recombinant DNA construct and growing the transformed plant with the recombinant DNA construct and growing the transformed plant which the recombinant DNA construct is useful for improving plant with the recombinant DNA construct is useful for producing plants with the improved plant properties, e.g. improved cold, heat or drought tolerance. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved plant growth and development under at least one stress content, improved plant growth and development under at least one stress condition, improved lignin production or improved glaatcomannan condition, improved lignin production or improved glaatcomannan condition, improved lignin production or improved dalactomannan condition. Note: The sequence data for this patent did not form part of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic communities.
                                                                                                                                                                                                                                                                                                  New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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                           CCTGCGCCAGCATTACGGGAATTAGATATGTCTTATGCCTGTAAATGCGATTTCTTTGTA
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                                                     367 CGCGCGCGGAAGATTTAAAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTTCAGCTT
                                                                                                                                             ProAlaProAlaAlaAlaAsnLeuAspProGluArgIleArgGlnValThrPheLeuVal
                                                                                                                                                                                                    CGCGCACCACCATCCTCGCTAGATAAAGGGCTGAACAATATTATTGTCACCATGGGC
                  AGCAACAGCATTCTGATCATCAAGGCGCCTAACAAGTTTCTCTCGCCGGAAGATATCGAT
                                                                                         GAAACGGTTTATCACGCAATAGAATTTGGCAAGAAACACGGGATTGAAGTGTTATTAAAC
                                                                                                                                                                 CCTAATGAAACCGAGCTGGAAATATTAACCGGTATGCCAGTGGATACCTATGACCATATT
                                                                                                                                                                                                                                          GAGAAAGGCGCCTGTGGATGACGCGTGACCAGGAAGTCCATGTTCCGGCGTTTAGAGTG
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HINKLE G J.
SLATER S C.
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant cauch as maize or soybean. The method of producing a transformed plant canced property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the coplynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plants with improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress conduction, this sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence date for this patent did not form, the form at norm, at noth, and the harmon provided the printed specification but was obtained in electronic
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                                                                                                                                                                                                      New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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                                                                                      Goldman
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CHEN X.
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183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                   204 ValhrgAlaAlaAsgSerLeuIleAlaArgGlyIleArgThrValIleValThrLeuGly
                            CCTGCGCCAGCATTACGGGAATTAGATATGTCTTATGCCTGTAAATGCGATTTCTTTGTA
                                                                                                                                                                                                                                                                                                                                                      727 AACGCTGTTGATACCAGCGCGCGCGCGATGCCTTTATCGGCTGTTTCGCGCATTACTAC
CGCGCGCGCGAAGATTTAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTTCAGCTT
                                                                                                       GAAACGGTTTATCACGCAATAGAATTTGGCAAGAAACACGGGATTGAAGTGTTATTAAAC
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| ProAlaProAlaAlaAlaAsnLeuAspProGluArgIleArgGlnValThrPheLeuVal
                                                                                                                                                                                                                                                                                                                       CCTAATGAAACCGAGCTGGAAATATTAACCGGTATGCCAGTGGATACCTATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                  607 CGCGCAGCGCCACGTTCGCTGGTAGATAAAGGGCTGAACAATATTATTGTCACCATGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 IleThrArgProGlyThrGlnLysAlaTyrAlaSerIleAspGlu 298
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L'maisonneuve J, Zhang Y, Jen S, Carter D;
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02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a canes. The disorders include SAPHO syndrome (synovitis, acne, puerulosis, Mypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies polypeptides may be used as antigens in the production of antibodies contactive therefore treat P. acnes infections. The acnes polypeptides and cherraning P. acnes presence, for example, by clasmostic agents for determining P. acnes presence, for example, by clasmostic agents for determining P. acnes presence, for example, by clasmostic agents form man activity of P. acnes presence for example, by chis patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at vaccinating against and diagnosing infections, especially useful for English 22062; 1069pp; treating acne vulgaris. SEQ ID NO 

Sequence 321 AA;

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GCGAACCAGGCCGTGGCGCCGCTAAGCTCAATTCAAAAGTATTGATGTTGACCAAAGTG 180
                                                                                                                                                    CCCAAAGAAGGGGAAACTCTGGAAGGGGCGGTTTAAAATCGGCTGCGGCAAAAGGG 120
                                                                                                                   18 MetAspileAlavalValGlySerAsnMetValAspLeulleSerTyrIleHisArgMet
                                                                                                          ATGGATATCGCGGTTATTGGCTCTAACATGGTGGACCTTATCACCTACACCAGATG
                                                                                                                                                               321
168
48
75
         Length:
Matches:
Conservative:
Mismatches:
                                                      Indels:
                                                               Gaps:
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          9.83e-85
                   831.50
73.97%
57.53%
52.30%
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Best Local Similarity:
Alignment Scores:
Pred. No.:
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300

|||:::||| ::: 98 ThrHisValLeuArgThrAsp---AlaSerGlyValAlaProllePheValAspPro 116

301 AACTCCAGCAACAGCATTCTGATCATCAAAGGCGCTAACAAGTTTCTCTCGCCGGAAGAT

360 136 420

361 ATCGATCGCGCGCGCAAGATTTAAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTT

421 CAGCTTGAAACGGTTTATCACGCAATAGAATTTGGCAAGAAACACGGGATTGAAGTGTTA

540

177 LeuAsnProAlaProValAlaProGluLeuAspLeuGluArgIleArgGlyIleGluPhe 196

TTAAACCCTGCGCCAGCATTACGGGAATTAGATATGTCTTATGCCTGTAAATGCGATTTC

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encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymuclectides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polymuclectide of the invention, antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention, a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. 216 9 236 720 256 780 840 296 invention relates to an isolated polynucleotide (ACF64435-ACF64733) :::||| :::||||||:::||| LeuGlySerArgGlyAlaMetTrpAlaHisAlaGluGlyArgLysIleIleLysAlaPro ATGGGCGAGAAAGGCGCGCTGTGGATGACGCGTGACCAGGAAGTCCATGTTCCGGCGTTT 721 AGAGTGAACGCTGTTGATACCAGCGCGCGGCGATGCCTTTATCGGCTGTTTCGCGCAT 257 valValGlnAlaValABpThrThrGlyAlaGlyABpAlaPheIleGlyCyBPheAlaLyB TTTGTACCTAATGAAACCGAGCTGGAAATATTAACGGGTATGCCAGTGGATACCTATGAC CATATTCGCGCAGCGCCACGTTCGCTGGTAGATAAAGGGCTGAACAATATTATTGTCACC ů Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL; Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter Barth B, Vallieve-Douglass J; Propionibacterium acnes predicted ORF-encoded polypeptide #22062. Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine. TTCAGCGTCACCGGGAAGGCACCCAATCCTTTAT 876 AspSerValThrArgHisGlyThrGlnSerSerTyr 308 Example 1; SEQ ID NO 22062; 1481pp; English. Ź ABM57386 standard; protein; 321 11-OCT-2002; 2002WO-US032727. 15-OCT-2001; 2001US-00978825. (first entry) Propionibacterium acnes. WPI; 2003-381789/36. N-PSDB; ACF64541. (CORI-) CORIXA CORP. WO2003033515-A1 20-OCT-2003 24-APR-2003 841 ABM57386; 197 601 199 237 781 297 541 ABMS7386 RESULT 셤 g 셤 ઠે 요 8 셤 셤 8 δ ò ઠે

continue cotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit cor detecting or determining the presence or absence of P, acnes in a patient; and a method for inhibiting the development of P, acnes in a continue to patient; and a method for inhibiting the development of P, acnes in a corp. Presenting cells that express the proteins. T cell populations or antigen-presenting cells that express the proteins. T cell populations or antigen-presenting cells that express the corp. The polymocleotides can also be used as probes or primers for uncleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P, acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present cadence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P, acnes polymocleotides of the cinvention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published\_pct\_sequences ACCIATGIAGAAAAAGIACCGIGIACCAGCAGCGCGIAGCGCCGATITICGICAACGCC 300 ||||:::||| ::: ThrHisValLeuArgThrAsp---AlaSerSerGlyValAlaProllePheValAspPro 116 480 176 CCCAAAGAAGGGGAAACTCTGGAAGCGCCGGCGTTTAAAATCGGCTGCGGCGGAAAAGGG 120 GGCGACGATATTTTGCCGACAACACCATTCGTAATCTCGAATCCTGGGGGATCAATACG 240 ATCGATCGCGCGCGGAAGATTTAAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTT 420 GCGAACCAGGCCGTGGCGGCCGCTAAGCTCAAATCAAAAGTATTGATGTTGACCAAAGTG 180 57 301 AACTCCAGCAACAGCATTCTGATCATCAAGGCGCTAACAAGTTTCTCTCGCCGGAAGAT CAGCTTGAAACGGTTTATCACGCAATAGAATTTGGCAAGAAACACGGGATTGAAGTGTTA TTANACCCTGCGCCAGCATTACGGGAATTAGATATGTCTTATGCCTGTAAATGCGATTTC 321 168 48 75 Conservative: Mismatches: Indels: Length: Matches: Gaps: (1-321)US-10-049-750-11 (1-921) x ABM57386 831.50 73.97% 57.53% 52.30% Percent Similarity: Best Local Similarity: Sequence 321 AA; Alignment Scores: 18 61 38 58 181 78 241 86 361 421 121 481 Query Match: DB: 8888888888888888888888888 셤 ò 셤 8 셤 ઠે g ò 요 셤 δ ò 셤 ò 셤 ઠે 8

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TTTGTACCTAATGAAACCGAGCTGGAAATATTAACCGGTATGCCAGTGGATACCTATGAC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polymptide from a microbial source. The invention also relates to a transformed plant transformed plant having an improved property. The plant is a crop plant transformed plant having an improved property. The plant is a crop plant baving an improved property comprises transformed plant thaving an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plants with improved plant properties, e.g. improved cold, heat or drought tolerance,
                      :::||| :::||||||:::|||
237 LeuGlySerArgGlyAlaMetTrpAlaHisAlaGluGlyArgLysIleIleLysAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA construct; transformed plant; improved plant property;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
 ATGGGCGAGAAAGGCGCGCTGTGGATGACGCGTGACCAGGAAGTCCATGTTCCGGCGTTT
                                                                                   721 AGAGTGAACGCTGTTGATACCAGCGGCGCGGCGATGCCTTTATCGGCTGTTTCGCGCAT
                                                                                                                                  TACTACGTCCAGAGCGGGATGTGGAAGCCGCCATGAAAAAGCCGTCCTCTTTGCCGCT
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                                                                                                                                                                                                                                                                                                      ADN25077 standard; protein; 304
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HINKLE G J.
SLATER S C.
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tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress ordition. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
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|GluthrVall1eHisThrValArgArgAlaAlaGlutrpGlyValArgThrIleLeuAsn
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235 GlyArgGlyAlaArgLeuValThrArgAlaGlyValValValProIleAlaProValArgVal
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Similarity:
Sequence 308 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, pseudomonas aeruginosa and Enterococcus facealla. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The bused to screen compounds in rational drug discovery programmes. The bused caids which are required for cell proliferation in a wide variety of organisms. The present sequence is also useful to screen for homologous cucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent electronic format directly from WIPO at the valous obtained in electronic format directly from WIPO at the valous obtained in the wipo int/pub/published_pot_sequences
727 AACGCTGTTGATACCAGCGCGCGCGATGCCTTTATCGGCTGTTTCGCGCATTACTAC 786
                                                                             294
              ThrProValAspThrThrGlyAlaGlyAspAlaPheIleGlyAlaPheLleu
                                                                 GTCCAGAGCGGGGATGTGGAAGCCGCCATGAAAAAAGCCGTCCTCTTTGCCGCTTTTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr GJ;
                                                                                                                                                                                                                                                                                             Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa cellular proliferation protein #251
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                                                                                                                                                                                       AAU36261 standard; protein; 308
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2000US-020727P.
2000US-0242578P.
2000US-0253625P.
2000US-0253625P.
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Xu HH;
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23-MAY-2000;
26-MAY-2000;
23-0007-2000;
27-DEC-2000;
16-FEB-2001;
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Yamamoto RT,
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|GluThrValGlyHisValLeuArgArgAlaHisAlaLeuGlyLysThrValIleLeuAsn 164
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LysAlaLeuAspThrThrAlaAlaGlyAspThrPheValGlyGlyPheAlaAlaAlaLeu 264
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5 ValLeuValValGlySerLeuAsnMetAspLeuValValArgAlaProArgLeuProArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                667 GAGAAAGGCGCGCTGTGGATGACGCGTGACCAGGAAGTCCATGTTCCGGCGTTTAGAGTG
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122
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                      Matches:
Conservative:
Mismatches:
Indels:
       ength:
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9.41e-53
550.00
59.33*
42.00*
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300 GlnAsnAlaIleValIleValAlaGlyGlyAsnGlyHisLeuSerProAlaValLeuAla
                                                                                                                                                                                                                                                  400 GlyArgAlaAlaGluArgLeuArgGluMetGlyAlaGlyArgValIleValThrLeuGly
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420 AlaGinGlyAlaLeuLeuValGlyGluGlyArgValGluHisPheProValAlaArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human transferase; HTFS; agonist; antagonist; cellular signalling; proliferation; cell proliferative disorder; immune disorder; atheroscelerosls; hepatitis; psoriasis; cancer; tumour; inflammation; AIDS; Addison's disease; allery; asthma; anaemia; cirrhosis; crohn's disease; atopic dermatitis; diabetes mellitus; multiple sclerosis; rheumatoid arthritis; pancreatitis; systemic lupus erythematosus; thrombocytopenia; ulcerative colitis; haemodialysis; extracorporeal circulation; trauma; transgenic animal;
                                                               280 ValGluArgValAlaGlyGluSerSerGlyValAlaLeuIleValValAspAspSerSer
                                                                                                                                                                                                                                                                                                                                                        CCTGCGCCAGCATTACGCAATTAGATATGTCTTATGCCTGTAAATGCGATTTCTTTGTA
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                                              GATATITITGCCGACAACACCATTCGTAATCTCGAATCCTGGGGGATCAATACGACGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therappy of pathological conditions, as molecular traspets for diagnosis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P aeruginosa nucleic acid, as components of effective antibacterial targets, as templates for antibacterial dargs, including anti-P. aeruginosa-derived peptides or polypeptides, components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences AB067826-C. RB084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 CAGGCCGTGGCGGCCGCTAAGCTCAATTCAAAGTATTGATGTTGACCAAAGTGGCGGC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
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200 ValLeuValValGlySerLeuAsnMetAspLeuValValArgAlaProArgLeuProArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 GlyGlyGluThrLeuAlaGlyGlnSerPheThrThrIleProGlyGlyLy8GlyAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ATCGCGGTTATTGGCTCTAACATGGTGGACCTTATCACCTACACCAAACCAGATGCCCAAA
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                                                                                                                                          Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
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Conservative:
Mismatches:
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                                                                                                               Pseudomonas aeruginosa polypeptide #15311.
                                                                                                                                                                                                                                                                                                                                                                         Rubenfield MJ, Nolling J, Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
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                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP
                   ABO83136 standard; protein; 503
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59.14%
41.86%
34.53%
                                                                                 entry)
                                                                                                                                                                          Pseudomonas aeruginosa.
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Best Local Similarity:
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useful as molec
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27-JUL-1998;
                                                                               29-JUL-2004
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                                                 AB083136;
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GAAGGGGAAACTCTGGAAGCGCCGGCGTTTAAAATCGGCTGCGCCGGAAAAGGGGCCGAAC

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127 CAGGCCGTGGCGCCGCTAAGCTCAATTCAAAGTATTGATGTTGACCAAAGTGGGCGAC 186
                                                                                                               38 ThrGlydluThrIleHisGlyHisLysPhePheIleGlyPheGlyGlyLysGlyAlaAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAB73494-AAB73515 represent novel human transferase proteins HTFS-1 to HTFS-42, and sequences AAH23801-AAH23812 represent cDNAs encoding them. The proteins play important roles in the regulation of cellular signalling and proteins play important roles in the regulation of cellular signalling and proteins play important roles in the regulation of cellular signalling and proteins play important roles in the regulation of cellular signalling and proteins play ind to an HTFS protein.

Compositions which modulates the activity of an HTFS protein. HTFS protein.

Compositions of genetic construct encoding an HTFS protein, HTFS agonist or antagonist, or genetic construct encoding an HTFS protein are useful for treating a disease or condition associated with decreased or increased expression of functional HTFS. Disorders which may be treated using such compositions include cell proliferative disorders and immune disorders.

Compositions include cell proliferation, AIDS, Addison's disease, brain and uterus cancer), inflammation, AIDS, Addison's disease, cancers, inflammation, and and immune disease, atopic dermatitis, disbetes mellitus, multiple sclerosis, thematolia archaritis, partemic lupus erythematosus, thrombocytopenia, and cancer, haemodialysis, extracorporeal circulation, trabuma and composition probes encoding HTFS proteins are useful for creating transgenic cancer, haemodialysis, extracorporeal circulation, level and to generate or hybridisation probes useful in mapping the naturally occurring genomic sequences. HTFS, and its catalytic or immunogenic fragments are useful for screening techniques. Antibodies which specifically bind HTFS may be 
                                                                                                                                                                                                                                                                                                                                                                        for diagnosis,
                                                                                                                                                                                                                                                                                                                                                                    Human transferase polypeptides and polynucleotides useful for dia
prevention and treatment of cell proliferative and immune system
disorders and for identifying agonists and antagonists.
                                                                                                                                                                                                                                                          Lal P, Bandman O, Patterson C;
Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 133-134; 157pp; English.
                                                                                                                                                                                                                                                          Yue H, Hillman JL,
Azimzai Y, Lu DAM,
                                                                                                                                              02-NOV-2000; 2000WO-US030485.
                                                                                                                                                                                   99US-0163595P
gene therapy; drug screening
                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.74e-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 322 AA
                                                                       WO200132888-A2
                                    Homo sapiens
                                                                                                                                                                                   04-NOV-1999;
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Shih LL,
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99
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1117
557
1117
Length:
Matches:
Conservative:
Mismatches:
                                 Indels:
                                                        US-10-049-750-11 (1-921) x AAB73533 (1-322)
      546.00
58.98%
39.66%
34.34%
              Percent Similarity:
Best Local Similarity:
                                Query Match
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CN1342697-A.

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427 GAAACGGTTTATCACGCAATAGAATTTGGCAAGAAACACGGGATTGAAGTGTTATTAAAC 486
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                                                                                                   187 GATATTTTGCCGACAACACCATTCGTAATCTCGAATCCTGGGGGGATCAATACGACGTAT 246
                                                                             247 GTAGAAAAAGTACCGTGTACCAGCAGCGGCGTAGCGCCGATTTTCGTCAACGCCAACTCC 306
                                                                                                                                                        307 AGCHACAGCATTCTGATCATCAAAGGCGCTAACAAGTTTCTCTCGCCGGAAGATATCGAT 366
                                                                                                                                                                                                                                     367 CGCGCGGCGGAAGATTTAAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTTCAGCTT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        547 CCTAATGAAACCGAGCTGGAAATATTAACCGGTATGCCAGTGGATACCTATGACCATATT 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 GlyGluAlaAlaLeuValLeuLeuLysArgGlyCysGlnValValIleIleThrLeuGly 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :::|||
238 AlaGluGlyCysValValLeuSerGlnThrGluProGluProLysHisIleProThrGlu 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAC----TACGTCCAGAGCGGGGATGTGGAAGCCGCCATGAAAAAAGCCGTCCTCTT 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 TyrLeuAlaTyrTyrProAsnLeuSerLeuGluAspMetLeuAsnArgSerAsnPhelle 297
                      Human; protein 35.42; pfkB protein family; tumour; infection; dementia; embryonic development disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 607 CGCGCAGCGCCACGTTCGCTGGTAGATAAAGGGCTGAACAATATTATTGTCACCATGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  667 GAGAAAGGC-----GCGCTGTGGATGACGCGTGACCAGGAAGTCCATGTTCCGGCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAGTGAACGCTGTTGATACCAGCGCGCGCGATGCCTTTATCGGCTGTTTCGCGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   178
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The present invention relates to a polynucleotide for preventing, treating or diagnosing a disease in an individual. The composition or the polypeptide, polynucleotide or RNA precursor, or antibody is useful for diagnosing, preventing or treating diseases (e.g. cell proliferative diseases such as cancer) in an individual. These may also be used for identifying substances capable of binding to or modulating the function of the polypeptide, capable of affecting the function of the corresponding gene, or capable of inhibiting the cell division cycle or cell cycle progression, preferably mitosis and/or meiosis. The present sequence represents an antagonist of cell cycle progression protein
                                                                                                                                                                                       780
                                                                                           237
                                                                                                                                                    :::|||
238 AlaGluGlyCygValValLeuSerGlnThrGluProGluProLygHisIleProThrGlu 257
                                                                                                                                                                                                                                                    834
                                                                                                                                                                                                                                                                      cycle
GAGAAAGGC-----GCGCTGTGGATGACGCGTGACCCAGGAAGTCCCATGTTCCGGCGTTT
                                                                                                                                                                                       AGAGTGAACGCTGTTGATACCAGCGCGCGGCGATGCCTTTATCGGCTGTTTCGCGCAT
                                                                                                                                                                                                                                                   TAC-----TACGTCCAGAGCGGGGATGTGGAAGCCGCCATGAAAAAGCCGTCCTTT
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                                                              CGCGCAGCGCCACGTTCGCTGGTAGATAAAGGGCTGAACAATATTATTGTCACCATGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cell cycle progression genes and proteins for modulating cell c progression in cells, for preventing, treating or diagnosing cell proliferative diseases (e.g. cancer) or for identifying modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; cancer; cell division cycle; mitosis; meiosis; cell cycle progression.
                                                                                                                                                                                                                                                                                                                 GCCGCTTTCAGCGTCACCGGGAAAGGCACCCAATCCTCTTATCCA 879
                                                                                                                                                                                                                                                                                                                                  Antagonist of cell cycle progression polypeptide #152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ပဲ
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                                                                                                                                                                                                                                                                                                     The present sequence represents human protein 35.42 containing pfkB protein family characteristic sequence fragments (1). Also described is method for preparing (1) using DNA recombination technology. (1) can be used for treating embryonic development disorders, tumours, infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||||||::
ThrGlyGluThrIleHisGlyHisLysPhePheIleGlyPheGlyGlyLysGlyAlaAsn
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AspSerPheGlyAsnAspTyrIleGluAsnLeuLysGlnAsnAspIleSerThrGluPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein 35.42 containing pfkB protein family characteristic sequence fragment and encoding polynucleotide, useful for treating embryonic development disorder, tumor, infection and dementia.
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Indels:
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Matches:
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238 AlaGluGlyCysValValLeuSerGlnThrGluProGluProLy8HisIleProThrGlu 257
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                                                                                                         667 GAGAAAGGC-----GCGCTGTGGATGACGCGTGACCAGGAAGTCCATGTTCCGGCGTTT
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Sequence 5777, Application US/09543681A

Batent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

SEQ ID NO 5777

LENGTH: 311
Sequence 3946, App
Sequence 786, App
Sequence 3900, App
Sequence 5214, App
Sequence 7111, App
Sequence 6, Appli
Sequence 7264, App
Sequence 7264, App
                                                                                                                                                                     Sequence 1358, A Sequence 1358, A Sequence 17, Appli Sequence 2, Appli Sequence 2, Appli Sequence 34, Appli Sequence 10221, A Sequence 102757, A Sequence 10377, A Sequence 10377, A Sequence 7458, Appli Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CCCAAAGAAGGGGAAACTCTGGAAGCGCCGGCGTTTAAAATCGGCTGCGGCGGAAAAGGG 120
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Sequence 4423, Ap
Sequence 32984, A
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Sequence 3
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US-09-1104-010C-5214

US-09-134-001C-5214

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US-09-543-6BA-7111

US-09-489-019A-13558

US-09-489-019A-13558

US-08-816-611-2

US-09-918-249-4

US-08-918-249-4

US-08-918-249-4

US-08-918-249-4

US-09-345-603-4

US-09-345-603-4

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US-09-918-105-125-1

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US-09-189-019A-125-1

US-09-1107-532A-6336

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-MODEL=frame+ n2p.model -DFV=xlp
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-Q=/Cogn2_1/(SPTO 500-1)p/US10049750/runat_23122005_113553_6317/app_query.fasta_1.1742
-DB=ISBAUEd_Patents AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -TRR MINS=0 -ALIGN=15
-MODE=LCOAL. -OUTFWT=pto -NOFM=ext -HEAPSIZE=500 -MINIMENE -MAXLEN=200000000
-USER=US10049750_@CGN 1 1.101 @runat_23122005_113553_6317 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WALT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5983, Ap
Sequence 14043, Ap
Sequence 14043, A
Sequence 7221, Ap
Sequence 7214, Ap
Sequence 7290, Ap
Sequence 7290, Ap
Sequence 4524, Ap
Sequence 4524, Ap
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Sequence 31882, A
                                                                                                                                   December 23, 2005, 22:17:41; Search time 37.391 Seconds (without alignments) 4072.865 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                     - protein search, using frame_plus_n2p model
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US-09-252-991A-31882
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US-09-710-279-3062
US-09-134-001C-4521
US-09-543-681A-8124
US-09-543-681A-8124
US-09-489-039A-9668
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US-09-543-681A-8124
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307 AGCAACAGCATTCTGATCATCAAAGGGGCTAACAAGTTTCTCTCGCGGAAGATATCGAT 366
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|GlnAsnAlaIleValIleValAlaGlyGlyAsnGlyHisLeuSerProAlaValLeuAla 319
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280 ValGluArgValAlaGlyGluSerSerGlyValAlaLeulleValValAspAspSerSer
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260 AspalaTyrGlyAspGlnLeuTyrArgAlaLeuGlnAlaGluGly1leAspCysGlnGly
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Mismatches:
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Matches:
                                                                                                                                                           Indels:
                                      TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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 NOS:
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Best Local Similarity:
                                                                US-09-252-991A-31882
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LENGTH: 503
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Patent No. 6551795
GENERAL INFORMATION:
FOR INVENTION:
GENERAL INFORMATION:
TITLE OF INVENTION:
AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
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                           121 GCGAACCAGGCCGTGGCGGCCGCTAAGCTCAATTCAAAAGTATTGATGTTGACCAAAGTG
                                                                               GGCGACGATATTTTGCCGACAACACCCATTCGTAATCTCGAATCCTGGGGGATCAATACG
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                                         CAGCTTGAAACGGTTTATCACGCAATAGAATTTGGCCAAGAAACACGGGATTGAAGTGTTA
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US-09-252-991A-31882
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Patent No. 6703492
GENERAL INFORMATION:
TATLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT PILING DATE: 1000-11-09
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
            215 GlyAlaAlaLysAlaAlaAsnIleLeuHisSerLysGlyIleLysHisValLeuIleThr
                                                                                                                                               :::||| :::|||
LeuGlySerArgGlyValTrpPheSerGluGlnGlyThrGlyMetIleIleProGlyPhe
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Conservative:
Mismatches:
Indels:
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ORGANISM: Artificial Sequence
FEATURE:
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458.00
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35.76%
28.81%
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3062
LENGTH: 302
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315 PheLeuAla 317
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                Sequence 3637, Application US/09543681A

Patent No. 6665709

GENERAL INFORMATION:

APPLICANT: GARY BRETON:

TITLE OF INVENTION:

DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 5983

LENGTH: 320
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               38 ProGlyGluThrVallleGlyHisAspTyrLysIleAlaPheGlyGlyLysGlyAlaAsn
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Best Local Similarity:
                                                       907 TCG 909
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US-09-543-681A-5983
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724 GIGAACGCIGITGAIACCAGCGGGGGGGGGAIGCCITTAICGGCTGTTCGCGCAITAC 783
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                                                                                                                                 GAAGGGGAAACTCTGGAAGCGCCGGCGTTTAAAATCGGCTGCGGCGGAAAAGGGGCGAAAC
                                                                                                                                                                                                                                                                                                                             307 AGCAACAGCATTCTGATCAACAAGGCGCTAACAAGTTTCTCTCGCCGGAAGATATCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          844 AGCGTCACCGGGAAAGGCACCCCAATCCTTATCCAAGCATTGAGCAATTTAATGAGTAT
                                                                                                                                                                                CAGGCCGTGGCGGCCGCTAAGCTCAAATTCAAAAGTATTGATGTTGACCAAAGTGGGCGAC
                                                                                                                                                                                                                                88 AspAspIleGlyGluArgIleArgArgGlnLeuAlaSerAspLysIleAspValAlaPro
                                                                                                                                                                                                                                                                                                                GTAGAAAAAGTACCGTGTACCAGCAGCGGCGTAGCGCCGATTTTCGTCAACGCCAACTCC
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                                                                                                                    ATCGCGGTTATTGGCTCTAACATGGTGGACCTTATCACCTACACCAAACCAGATGCCCAAA
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                    Matches:
Conservative:
Mismatches:
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          3.19e-43
452.50
53.31%
36.75%
28.46%
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LeuAla 327
                                  Percent Similarity:
Best Local Similarity:
Alignment Scores:
Pred. No.:
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Patent No. 6610836
GENERAL INFORMATION
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 14043
LENGTH: 330
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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220 GlyGluGlnGlyThrTyrCysAlaTyrGlnGluGlnTyrLysMetIleProAlaCysAsn 239
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81 TyrIleLeuThrSerGluSerGluGluThrGlyGlnAlaPheIleThrValAspGluAla 100
                                                                                                         304 TCCAGCAACAGCATTCTGATCATCAAAGGCGCTAACAAGTTTCTCTCGCCGGAAGATATC 363
                                                                                                                                                         GATCGCGCGCGCAAAAATTAAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTTCAG 423
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GluMetSerAlaAspAlaPheIleGlyAlaAspPheValValAlaGlnLeuGluValPro 140
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           GACGATATITITGCCGACACACCCATTCGTAATCTCGAATCCTGGGGGATCAATACGACG 243
                                                          TATGTAGAAAAAGTACCGTGTACCAGCAGCGCGTAGCGCCGATTTTCGTCAACGCCAAC 303
                          781 TACTACGTCCAGAGCGGGGATGTGGAAGCCGCCATGAAAAAAGCCGTCCTTTTGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    941 TTCAGCGTCACCGGGAAAGGCACCCAATCCTCTTATCCAAGCATTGAGCAATTTAAT---
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US-09-489-039A-14043
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RESULT 7

US-09-543-681A-7498

US-09-543-681A-7498

Sequence 7498, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIT

TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: UNMERR: US 60/128,706

PRIOR PEDLICATION UNMERR: US 60/128,706

PRIOR PEDLICATION UNMERR: US 60/128,706

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 7498
                                                                                                                                                                         |||||||:::|||
233 GlyGluGlnGlyThrTyrCysAlaTyrGlnGluGlnTyrLysMetlleProAlaCysAsn 252
                                                                                                                                                                                                                                  781 TACTACGICCAGAGGGGGATGIGGAAGCCGCCAIGAAAAAAGCCGICCICTIIGCCGCT 840
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                  273 LeuAsnLysAspLeuSerAsnLeuGluSerAlaIleArgLeuAlaAsnGlnAlaSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          604 ATTCGCGCGCGCGCCACGTTCGCTGGTAGATAAAGGGCTGAACAATATTATTGTCACCATG
                                                                             GCCCACAAAGCCCCCCTCTGCATGACGCCTGACCAGGAAGTCCATGTTCCGGCGTTTAGA
                                                                                                                                                      GTGAACGCTGTTGATACCAGCGCGCGCGCGATGCCTTTATCGGCTGTTTC---GCGCAT
                                                                                                                                                                                                                                                                                                             841 TTCAGCGTCACCGGGAAAGGCACCCAATCCTCTTATCCAAGCATTGAGCAATTTAAT---
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Mismatches:
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Best Local Similarity:
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Pred. No.:
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                                              Sequence 4521, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
GENERAL OF INVENTION:
FILE OF INVENTION:
GENERAL APPLICATION NUMBER: US 60/064,964
FRICH APPLICATION NUMBER: US 60/064,964
FRICH RELING DATE: 1997-11-08
FRICH RELING DATE: 1997-08-14
FRICH FILING DATE: 1997-08-14
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94 TyrIleLeuThrSerGluSerGluGluThrGlyGlnAlaPhelleThrValAspGluAla 113
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114 GlyGlnAsnThrIleLeuValTyrGlyGlyAlaAsnMetThrLeuSerAlaThrAspVal 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGGGAAACTCTGGAAGCG---CCGGCGTTTAAAATCGGCTGCGGCGGAAAAGGGGGCG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 GACGATATTTTGCCGACAACACCATTCGTAATCTCGAATCCTGGGGGATCAATACGACG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 TATGTAGAAAAAGTACCGTGTACCAGCAGCGCGTAGCGCCGATTTTCGTCAACGCCAAC 303
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US-09-134-001C-4521
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US-09-134-001C-4521
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RESULT 9
US-09-9668
US-09-489-039A-9668
Sequence 9668, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION
APPLICANT: GAPY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
                                                                                                                                CAGGCCGTGGCGGCCGCTAAGCTCAAAAGTATTGATGTTGACCAAAGTGGGCGAC 186
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GlySerLysGlySerLeuAlaTyrAspGlyTyrLysTyrIleTyrSerProAlaTyrPro 332
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                                        GATATITITGCCGACAACACCATICGTAATCTCGAATCCTGGGGGATCAATACGACGTAT 246
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AspGlnPheSerAspTyrAlaValAsnPheIleSerSerSerArgIleLysThrSerThr 173
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                                                                                                                                                                                                                                                          AGCAACAGCATTCTG---ATCATCAAAGGCGCTAACAAGTTTCTCTCGCCGGAAGATATC 363
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-10-049-750-11 (1-921) x US-09-543-681A-8124 (1-406)
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Patent No. 6605709
GENERAL INFORMATION:
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TITLE OF INVENTION:
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TITLE OF INVENTION:
FILE REPRENCE: 2709-1002-001
CURRENT FILING DATE: 2000-04-05
PRIOR PELLORION NUMBER: US 60/128,706
PRIOR PELLORION DATE: 1999-04-09
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287 AlaValThrArgAlaGlyAlaGlnProSerValProTrpArgHisGluIleGluAlaPhe 306
                              109 GluAsnValIleGlyIleHisAlaGlyAlaAsnGlyArgLeuAsnArgGluTyrValGlu 128
                                                                                                                       GAAACGGTTTATCACGCAATAGAATTTGGCAAGAAACACGGGATTGAAGTGTTATTAAAC 486
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Matches:
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ORGANISM: Klebsiella pneumoniae
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US-09-489-039A-7290
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TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/489, 039A CURRENT FILING DATE: 2000-01-27 PRIOR PILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342 SEQ ID NO 9668 LENGTH: 342
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Matches:
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Mismatches:
Indels:
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Pred. No.:
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Squence 7290, Application US/09489039A

Factor 10. 6610836

GENERAL INFORMATION:

APPLICANT: GAIV BRECON et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFRENCE: 2709.2004001

FILE REPRENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR RPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
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Sequence 4841, Application US/09543681A

Patent No. 6605709

Patent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 4841
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341 LysHisLeuPheMetAspAlaSerPheCysLeuIleGlnThrGluIleFroLeuSerAla 360
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        GTGGCGGCGCTAAGCTCAATTCAAAGTATTGATGTTGACCAAAGTGGGCGACGATATT 192
                                                                                          AAAGTACCGTGTACCAGCAGCGCGTAGCGCCGATTTTCGTCAACGCCAACTCCAGCAAC 312
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493 SerValSerLygGluGlyValIleAspSerLeuValAspHisValThrLeuGluAsnTyr
                                                                      193 TTTGCCGACAACACCATTCGTAATCTCGAATCCTGGGGGATCAATACGACGTATGTAGAA
                                                                                                                                                                                                    373 GCGGAAGATTTAAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTTCAGCTTGAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               604 ATTCGCGCAGCGGCACGTTCGCTGGTAGATAAAGGGCTGAACAATATTATTGTCACCATG
                                                                                                                                                                                                                                                                                                                                GTTTATCACGCAATAGAATTTGGCAAGAAACACGGGATTGAAGTGTTATTAAACCCTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          784 TACGICCAGAGCGGGGATGIGGAAGCCGCCATGAAAAAAGCCGICCTCTTIGCCGCTITIC
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US-09-543-681A-4841
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US-09-134-00C-4524

j Sequence 4524, Application US/09134000C

patent No. 6617156

GENERAL INFORMATION:

APPLICATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: US-032

CURRENT FILING DATE: 1998-08-13

CURRENT FILING DATE: 1998-08-13

PRIOR PELICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

LENGTH: 529
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                                                                   TTAAACCCTGCGCCAGCATTACGGGAATTAGATATGTCTTATGCCTGTAAATGCGATTTC 540
                                                                                                           541 TTTGTACCTAATGAAACCGAGCTGGAAATATTAACCGGTATGCCAGTGGATACCTATGAC 600
                                                                                                                                                                                                                                                                                                                                                                     CATTACTACGTCCAGAGCGGGGATGTGGAAGCCGCCATGAAAAAGCCGTCCTTTTGCC 837
                                                                                                                                                                                                                                                                                                                                                                                                   279 TyrCysIleValAsnGlyPheSerLeuThrAspAlaIleProPheAlaAlaGluIleSer 298
                                                                                                                                                                                                                                                                                                                                                                                                                                   838 GCTTTCAGCGTCACCGGGAAAGGCACCCCAATCCTTTATCCAAGCATTGAGCAATTTAAT 897
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241 LysThrAsnPheLeuSerSerTyrAlaLysPheProGlyGlyLysGlyLeuAsnGlnAla
                                                                                                                                                                                                                                                                                                       TITAGAGTGAACGCTGTTGATACCAGCGCGCGCGATGCCTTTATCGGCTTTTCGCG
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221 ValValGlySerLeuAsnValAspAsnTyrLeuTyrSerThrAsnLeuProHisAsnGly
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                                                                                                                                                                                                                                         ATGGCCGAGAAAGGCCCCCTGTGCATGACGCGTGACCAGGAAGTCCATGTTCCGGCG---
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.72e-34
376.50
49.51%
31.80%
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Best Local Similarity:
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DB:
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Sequence 3946, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 ATTGAAGTGTTATTAAACCCTGCCAGCATTACGGGAATTAGATATGTCTTATGCCTGT 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 CAACTGGAAGTTCAGCTTGAAACGGTTTATCACGCAATAGAATTTGGCAAGAAACACGGG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 LysThrThrIleLeuAsnProAlaProAlaArgGluThrIleProThrGluLeuLeuGlu 42
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60
32
63
16
                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-049-750-11 (1-921) x US-09-107-532A-3946 (1-170)
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: «Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 14 July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHAX: (781)893-8277
TELECHAX: (781)893-8277
TELECHAX: (781)893-8277
TELECHATION FOR SEQ ID NO: 3446:
SEQUENCE CHARACTERISTICS:
"ENGTH: 170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...170
SEQUENCE DESCRIPTION: SEQ ID NO: 3946:
                                             ORGANISM: Enterococcus faecium
                      886 GAGCAATTTAATGAGTATCTTTCGTTG
                                                                                                                                                                                                                                                                                                                      STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 170 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
COUNTRY: USA
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250.00
53.80%
35.09%
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HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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Best Local Similarity:
                                                                                                                    US-09-107-532A-3946
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194 AspHisPheSerLysTyrAlaTyrLysTyrLeuGlnGluSerGlyIleAspSerPheThr 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ACGIATGTAGAAAAGTACCGTGTACCAGCAGCGCGTAGCGCCGATTTTCGTCAACGCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 ThrGlnAsnAsnIleThrAlaThrTyrLeuGlyAlaAsnAsnThrPheThrLeuGlnGlu 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 CAGCTIGAAACGGTTTATCACGCAATAGAATTIGGCAAGAAACACGGGATIGAAGTGTTA 480
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LyslleAlaAlaGlyGly------ThrMetProGluSerValLeuPheAlaSer 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 AspAlaLysGlnAlavalGluIleIleAlaGlyAsnGluLysLysLysValileIleTyr 351
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273 AsnileAspAlaAsnValLysAlaAlaSerPheAlaHisSerIleAsnLysThrValIle
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                                                                                                 451
87
61
146
15
                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                   Gaps:
                                                                                           1.1e-26
310.50
47.90%
28.16%
19.53%
                  mirabilis
                                                                                                                                       Percent Similarity:
Best Local Similarity:
TYPE: PRT
ORGANISM: Proteus
                                         US-09-543-681A-4841
                                                                               Alignment Scores:
Pred. No.:
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Sequence No. 6380370

Sequence No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-114

NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                 122 ------AspIleGlnValPheGlnAspAspIleLeuHisPhe---CysSerVal 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     675
                                                                                                                                                               ::: |||||| :::|||||| 102 AspPheSerPheTyrArgLysProSerAlaAspMetLeuTyrGlnProGluAsnlleAsp 121
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                                                                      253 AAAGTACCGTGTACCAGCAGCGCGTAGCGCCGATTTTCGTCAACGCCAACTCCAGCAAC 312
                                                                                               313 AGCATTCTGATCATCAAA-----GGCGCTAACAAGTTTCTCTCGCCGGAAGATATCGAT 366
                                                                                                                                                                                                                      367 CGCGCGGCGGAAGATTTAAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTTCAGCTT 426
                                                                                                                                                                                                                                                                                                                                   137 AspLeulleGluSerAspMetLysTyrAlaHisGluLysMetileGluLysPheGluSer 156
                                                                                                                                                                                                                                                                                                                                                                        ------GTGTTATTAAACCCTGCGCCAGCATTACGCGAATTAGATATGTCTTAT 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCTGTAAA-----TGCGATTTCTTTGTACCT---------AATGAA 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTGATACCAGCGCGCGAGCGATGCCTTTATCGCTTTTCGCGCATTACTACGTCCAG 792
                     272 SerargHisSerGluCysLysAspLeuPheLysGluLysGlyLysAspIleLeuAlaPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITGCCGACAACACCATTCGTAATCTCGAATCCTGGGGGATCAATACGACGTATGTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                            157 ValAspGlyThrIleValPheAspProAsnValArgLeuProLeuTrpGluAspLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           556 ACCGAGCTGGAAATATTAACCGGTATGCCAGTGGATACCTATGACCATATTCGCGCAGCG
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                                                                                                                                                                                                                                                                                              427 GAAACGGTTTATCACGCAATAGAATTTGGCAAGAAACACGGGATTGAA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 786, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION,
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STRAPYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
 AAATGCGATTTCTTTGTACCTAATGAAACCGAGCTGGAAATATTAACCGGTATGCCAGTG
                                                                            589 GATACCTATGACCATATTCGCGCAGCGGCACGTTCGCTGGTAGATAAAGGGCTGAACAAT
                                                                                                 ThrasphibabsnSerLeuValalaalaalaGluLysLeuHisGluLeuGlyIhr
                                                                                                                                                    649 ATTATTGTCACCATGGGCGAGAAAGGCGCGCTGTGGATGACGCGTGACCAGGAAGTCCAT
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83 ValileileThrLeuGlySerAlaGlyAlaPheTyrHisThrGluLysGluHisGlyIle
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|IleGlyGluAlaLeuIleAspPheIleProAsnValThrHisSerLysLeuLysAspVal
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                                                                                                                                                                                                                          CTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: amino acid sequence US-09-710-279-786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            868 TCCTCTTATCCA-----AGCATTGAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/710,279; CURRENT FILING DATE: 2000-11-09; PRIOR FILING DATE: 1000-11-09; PRIOR FILING DATE: 1999-11-09; NUMBER OF SEQ ID NOS: 4472; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 786; TENGTH: 319; TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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24.77%
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Best Local Similarity:
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US-09-710-279-786
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180 CysGlnArgThrIleAsnAlaPheIleProLysAlaHisIleValLysIleSerAspGlu 199
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104 AspPheSerPheTyrArgLysProSerThrAspMetLeuTyrGlnProGluAsn1leAsp 123
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200 GluLeuLeuPheIleThrGlyLysLysAsnGluAsp-------GluAlaIle 214
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9 IleGlyGluAlaLeuIleAspPheIleProAsnValThrHisSerLysLeuLysAspVal 28
                                                                                                                                                                                                                                                                                                                      29 Glu-------GlnPheSerArgGlnValGlyGlyAlaProCysAsnValAla 43
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Matches:
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Mismatches:
Indels:
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                        TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                  8.48e-18
233.00
43.87%
25.15%
                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                             ; ORGANISM: Stapm
US-09-134-001C-3900
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SEQ ID NO 3900
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US-10-238-075-1139

Sequence 1139, Application US/10238075

Sequence 1139, Application US/10238075

Publicaction No. US20030148324A1

GENERAL INFORMATION:

APPLICANT: I.N.S.E.R.M.

TITLE OF INVENTION: Bolymucleotides which are of nature B2/D+ A- and which are isola TITLE OF INVENTION: Bolymucleotides and of the FILE REFERENCE: BLANDINE

CURRENT APPLICATION NUMBER: US/10/238,075

CURRENT APPLICATION NUMBER: 0003145

PRIOR FILING DATE: 2000-03-10

NUMBER OF SEQ ID NOS: 1576

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1139
   7383, Ap
2625, Ap
7595, Ap
1394, Ap
13191, Ap
131013, A
20151, Ap
21153, A
21153, A
21060, Ap
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; ORGANISM: Escherichia coli
US-10-238-075-1139
   Percent Similarity:
Best Local Similarity:
Query Match:
   Alignment Scores:
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Sequence 11397, A
Sequence 14829, A
Sequence 15011, A
Sequence 7730, Ap
Sequence 208, App
Sequence 304, App
Sequence 5584, App
Sequence 5584, App
Sequence 5584, App
                                                                                                      December 23, 2005, 22:42:49; Search time 162.356 Seconds (without alignments) 4740.464 Million cell updates/sec
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6: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                               OM nucleic - protein search, using frame_plus_n2p model
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US-10-369-493-730
US-09-815-242-11854
US-10-781-581-208
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US-10-786-493-5584
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Conservative:
Mismatches:
Indels:
CURRENT APPLICATION NUMBER: US/10/369,493;
CURRENT FILING DATE: 2003-02-28;
PRIOR APPLICATION NUMBER: US 60/360,039;
PRIOR FILING DATE: 2002-02-21;
NUMBER OF SEQ ID NOS: 47374;
SEQ ID NO 11397;
LENGTH: 298;
TYPE: PRT
ORANISM: Agrobacterium tumefaciens
US-10-369-493-11397
                                                                                                                           Length:
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US-10-369-493-11397
US-10-369-493-11397
Sequence 11397, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Glater, Steven C.
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (FILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES)
FILE REFERENCE: 38-10(52052)
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; Sequence 14029, Application US/10369493
; Publication No. USZ0030233675A1
; Publication No. USZ0030233675A1
; Sublication No. USZ0030233675A1
; Sublication No. USZ0030233675A1
; APPLICANT: Cao, Yongwei
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10 (52052) B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT PILING DATE: 2003-02-28
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14829
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US-10-369-493-14829
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Greyory J.
APPLICANT: Hinkle, Greyory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052)8
FILE REPERENCE: 38-10 (52052)8
FILE REPERENCE: 38-10 (52052)8
FILE REPERENCE: 38-10 (5305) 493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14281
LENGTH: 298
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Publication No. US20030233675A1
GENERAL INFORMATION:
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CRGANISM: Agrobacterium tumefaciens
US-10-369-493-14281
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Seven C.
APPLICANT: Goldman, Barry C.
APPLICANT: Goldman, Barry C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
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Sequence 15011, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
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SEQ ID NO 15011
LENGTH: 298
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Best Local Similarity:
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235 GlyArgGlyAlaArgLeuValThrArgAlaGlyValValProIleAlaProValArgVal
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION WINBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-01-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-02-16
PRIOR PILING DATE: 2000-03-16
PRIOR PILING 
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                                                                                  APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES
FILE REFREENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7730
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LOCATION: (1)..(304);
CTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-7730
               Sequence 7730, Application US/10369493
Publication No. US20030233675A1
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|GlnAsnAlaIleValIleValAlaGlyGlyAsnGlyHisLeuSerProAlaValLeuAla 124
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AlaArgGlyLeuAspGluAlaAlaAlaIleArgPheGlyGlnAlaAlaAlaAlaIleSer
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AlaGinGiyAlaLeuLeuValGiyGiyGiyArgValGiuHisPheProValAlaArgVal
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Publication No. US20050019746A1

GENERAL INFORMATION:

APPLICANT: Elex Therapeutics Ltd.

APPLICANT: Seery, Liam

APPLICANT: Murphy, Finbarr

TITLE OF INVENTION: Apoptosis-Related Kinase/GPCRs

FILE REFERENCE: 8912/2015

CURRENT APPLICATION NUMBER: US/10/781,581

CURRENT FILING DATE: 2004-02-18
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238 AlaGluGlyCysValValLeuSerGlnThrGluProGluProLysHisIleProThrGlu 257
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AspSerPheGlyAsnAspTyrlleGluAsnLeuLysGlnAsnAspIleSerThrGluPhe
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118 GlmasnIleIleVallleValAlaGlyAlaAsnLeuLeuLeuAsnThrGluAspLeuArg
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|GlyGluAlaAlaLeuValLeuLeuLysArgGlyCysGlnValVallelleThrLeuGly
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PRIOR APPLICATION NUMBER: US 10/764,238
PRIOR FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US 60/457,533
PRIOR APPLICATION NUMBER: UK 0301566.6
PRIOR FILING DATE: 2003-01-23
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn version 3.2
SEQ ID NO 208
LENGTH: 322
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546.00
58.98%
39.66%
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238 AlaGluGlyCysValValLeuSerGlnThrGluProdluProLyBHisIleProThrGlu 257
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APPLICANT: Graces
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gladman, Barry S.
APPLICANT: Gladman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERIES
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERIES
FILE REFERENCE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR PLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5584
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ORGANISM: Caenorhabditis elegans
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Best Local Similarity:
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US-10-369-493-5584
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78 AspSerPheGlyAsnAspTyrlleGluAsnLeuLysGlnAsnAspIleSerThrGluPhe 97
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                                                                                                              GENERAL INFORMATION:

APPLICANT: Glover, David
APPLICANT: Glover, David
APPLICANT: Glover, David
APPLICANT: Bell, Graham
APPLICANT: Bell, Graham
APPLICANT: Midgley, Carol
TITLE OF INVENTION: Call Cycle Progression Proteins
FILE REFERENCE: P01581940 CYK
CURRENT APPLICATION NUMBER: US/10/745,237
CURRENT FILING DATE: 2003-12-23
PRIOR FILING DATE: 2003-01-10
PRIOR PILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 600
SOFTWARE: PatentIn version 3.1
SEQ ID NO 304
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Indels:
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US-10-745-237-304
US-10-745-237-304
; Sequence 304, Application US/10745237
; Publication No. US20050227301A1
; GENERAL INFORMATION:
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US-10-745-237-304
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Best Local Similarity:
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Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                           GATATTTTTGCCGACACACCATTCGTAATCTCGGAATCCTGGGGGGATCAATACGACGTAT 246
                                                                                                         307 AGCAACAGCATTCTGATCATCAAAGGCGCTAACAAGTTTCTCTCGCCGGAAGATATCGAT 366
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LysGlyAsnArgAlaPheGluIleAlaArgSerHisGlyValThrThrPheLeuAsn 196
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GlyLyBGlyValLeuLeuAlaSerLyBGlyValABpABpValGluHi8ThrAlaValIle 276
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HisLeuvalAlaGlyHisProlleSerAlaSerIleArgSerAlaAlaAsnLeuAlaAla 316
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317 LeuSerValThrArgHisGlyThrGlnSerSerTyrTrpLysLeuAspGlulleArgGln 336
126
                                             CAGGCCGTGGCGCCCCTAAGCTCAAAAGTATTGATGTTGACCAAAGTGGGCGAC 186
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ProGlyGluSerValArgGlyHisAsnPheLysLeuGlySerGlyGlyLysGlyAlaAsn 76
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GAAGGGGAAACTCTGGAAGCGCCGCCGCCTTTAAAATCGGCTGCGGCGGAAAAGGGGCCGAAC
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146 IleaspalaalaMetargalaLeuGlullealaargGlyalaGlyValThrThrIleLeu
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Matches:
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12350
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37.29%
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US-10-369-493-12350
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| Sequence 4625, Application US/10369493
| Sequence 4625, Application No. US20030233675A1
| Sequence 4625, Application No. US20030233675A1
| GENERAL INPORMATION:
| APPLICANT: Cac, Yongwei
| APPLICANT: Chen, Xianfeng
| APPLICANT: Chen, Xianfeng
| APPLICANT: Chen, Xianfeng
| APPLICANT: Chen, Xianfeng
| TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
| TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
| TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
| TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
| TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
| TITLE OF INVENTION NUMBER: US 60/360,039
| PRIOR PLILING DATE: 2002-02-21
| NUMBER OF SEQ ID NOS: 47374
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261 AlaLeuAlaArgGlyAspAspAlaMetThrAlaLeuArgPheGlyCysAlaLeuAlaGly 280
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| LeuGlualaalaargargGlyLeuGluValalaargargHisGlyValIleThrValPhe 161
AspAlaIleGluAlaAspIleAlaAlaAlaArgValPheValThrGlnLeuGluGlnPro 141
                                                         CTTGAAACGGTTTATCACGCAATAGAATTTGGCAAGAAACACGGGATTGAAGTGTTATTA 483
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ORGANISM: Burkholderia fungorum
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Sequence 7383, Application US/10369493

Sequence 7383, Application William Wil
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                                                                               TTCAGCGTCACCGGGAAAGGCACCCAATCCTTATCCAAGCATTGAGCAATTTAATGAG 900
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63 AspAlaPheGlyAlaIleAlaArgAlaThrTrpAlaAlaGluGlyIle---ThrAlaArg 81
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US-10-369-493-7383
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Best Local Similarity:
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US-10-369-493-7383
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                                                                                                       CAGGCCGTGGCGGCCGCTAAGCTCAATTCAAAAGTATTGATGTTGACCAAAGTGGGCGAC 186
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::: ::::::|||||||::: valvallleLeuGlyIleTyrValThrAspLeuThrPheArgAlaGlyArgMetProGln 23
                                                              24 IleGlyGluThrIleAlaGlySerAlaPheAlaMetGlyProGlyGlyLysGlySerAsn 43
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64 AgpalaPheGlyAlaIleAlaArgAlaThrTrpAlaAlaGluGlyIle---ThrAlaArg 82
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Publication No. US20040009491A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
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78 AspSerPheGlyAsnAspTyr11eGluAsnLeuLysGlnAsnAspIleSerThrGluPhe
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PRIOR APPLICATION NUMBER: PCT/USO1/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: Patentin Ver. 3.1
ENG ID NO 2526
LENGTH: 299
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NAME/KEY: MISC_FEATURE
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                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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US-10-369-493-7595

i Sequence 7595, Application US/10369493

j Sequence 7595, Application US/10369493

j Publication No. US20030233675A1

general information

j APPLICANT: Cao, Yongwei

j APPLICANT: Hinkle, Gregory J.

APPLICANT: Gldman, Barry S.

APPLICANT: Gldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052) B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2003-02-28

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 7595

LENGTH: 300
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238 AlaGluGlyCysValValLeuSerGlnThrGluProGluProLy8HislleProThrGlu 257
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138 AlaAlaAlaAsnValIleSerArgAlaLysValMetValCysGlnLeuGlulleThrPro 157
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; ORGANISM: Burkholderia cepacia
US-10-169-493-7595
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127 CAGGCCGTGGCGGCCGCTAAGCTCAAAAGTATTGATGTTGACCAAAGTGGGCGAC 186
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223 AlaGlnGlyAlaTyrLeuLeuValGluGlyGlyGlyGlyArgHisPheProAlaProGln 242
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63 AspalaasnGlyAlaGlnArgValLysAspLeuGluValGluGlyIleAspCysSerGly
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GAAGGGGAAACTCTGGAAGCGCCGGCGTTTAAAATCGGCTGCGGCGGAAAAGGGGCGAAC
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Job time : 170.356 secs
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US-10-793-626-3062
; Sequence 3062, Application US/10793626
; Sequence 3062, Application No. US20050255478A1
; Publication No. US20050255478A1
; RENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 1999-11-09
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3062
Sequence 7660, Ap Sequence 2530, Ap Sequence 170, App Sequence 3702, Ap Sequence 170, App Sequence 1128, App Sequence 1128, App Sequence 2678, App Sequence 146, App Sequence 4486, App Sequence 4486, App Sequence 30, App Sequence 2, App 11
                                                                                                                                                                                                                                                                                                                      Sequence 2, Appli
Sequence 96, Appli
Sequence 721, App
Sequence 749, App
Sequence 249, App
Sequence 94, Appl
Sequence 96, Appl
Sequence 7096, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 4824, Ap
Sequence 7256, Ap
Sequence 1548, Ap
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JOTHER INFORMATION: Description of Artificial Sequence: synthetic
JCTHER INFORMATION: amino acid sequence
JCS-10-793-626-3062
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                                       US-11.055-822-170
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US-10-743-657-4486
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US-11-070-653-249
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US-11-070-653-249
US-11-070-653-26-1362
US-11-08-991-94
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ORGANISM: Artificial Sequence
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US09_NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US09_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                                 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

    protein search, using frame_plus_n2p model

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US-10-793-626-786
US-10-485-517-177
US-10-467-657-6514
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|AsnProAlaProAlaIle---GluLeuProLysSerLeuLeuGluLeuThrAspIleIle 179
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                                                                                      Sequence 786, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION: US20050255478A1
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ48002
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
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PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOUTHARE: PATENTIN VEY. 2.1
SEQ ID NO 786
LENGTH: 319
TYPE: PRT
CORGANISM: Artificial Sequence
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91 GCGTTTAAAATCGGCTGCGGGAAAAGGGGGCGAACCAGGCCGTGGCGGCCGCTAAGCTC 150
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GTACCTAATGAAACCGAGCTGGAAATATTAACCGGTATGCCAGTGGATACCTATGACCAT 603
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105 IleThrAsnLysAspGluThrGluThrTyrLeuAsnLeuLysIleGluSerThrAspAsp 124
                                                                     604 ATTCGCGCAGCGCACGTTCGCTGGTAGAGGGCTGAACAATATTATTGTCACCATG 663
                                                                                         GGCGAGAAAGGCGCGCTGTGGATGACGCGTGACCAGGAAGTCCATGTTCCGGCGTTTAGA 723
                                                                                                                                                            724 GIGAACGCIGII---GAIACCAGCGCGCGCGCGAIGCCIIIAICGCCIGIIICGCGCAI 780
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185 SerTrpLeuAsnGlyMetSerThrGluAspIleLeuIleAlaGlyMetValAsnAlaLys 204
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31 ThrTyrLysPhe---AlaGlyGlyLysGlylleAsnValSerArgValLeuLysThrLeu 49
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APPLICANT: Biospnexus incorporated
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REPERENCE: P100629WO
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-09
PRIOR FILING DATE: 2001-09
PRIOR FILING DATE: 2002-01-09
SOFTWARE: PATCHTIN VENEZORO-10-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: PATCHTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 185, Application US/10485517
Publication No. US20050256299A1
GAPPLICANT: University of Sheffield
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                                         GTTGATACCAGCGCGCGGCGATGCCTTTATCGGCTGTTTCGCGCATTACTACGTCCAG 792
                                                             ::: |||||||||| ::: |||:::::: ||| ::: ||| 47 SerHisLeuLeuLysLysAlaLysCysIleIleValAspLeuAsnLeuGlyLysGluAla 66
       232 AlaThrileTyrThrLygAgpAgpTyrArgileHigHigGluGlyTyrGlnValGlnAla 251
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Matches:
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                                                                                                                                                                                                                                                                                                                                                      Sequence 177, Application US/10485517
Fublication No. US200502562991
GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Foster, Simon
APPLICANT: Foster, Simon
APPLICANT: Poster, Simon
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629WO
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR APPLICATION NUMBER: GB 0200349.9
NUMBER OF SEQ ID NOS: 424
SEQ ID NO 177
LENGTH: 238
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312 LysGluAspIleLysAspTyr 318
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ORGANISM: Staphylococcus aureus
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------AlaTyrAlaGlnIleAlaGlnIleThrAlaGlnThr----- 154
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50 AspValGluSerThrAlaLeuGlyPheAlaGlyGlyPheProGlyLysPheIleIleAsp 69
                                                            ----AAAGTACCG-----
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APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
ITILE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR PILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMin99, version 1.04
SEQ ID NO 6514
                                     205 ACCATTCGTAATCTCGAATCCTGGGGGATCAATACGACGTATGTAGAA
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ORGANISM: Neisseria gonorrhoeae
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US-10-467-657-6514
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US-10-467-657-6514
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202 ValAlaAlaLeuThrArgLeuLeuLeuProAspThrAspIleLeuThrProAsnLeuPro 221
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302 ThralaGluLeuAlaLysGlyLeuAspValCysLysAlaValGlnThrAlaLysAlaTyr 321
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| Sequence 10. Application US/10467962B
| Publication No. US20050246784A1
| GENERAL INFORMATION:
| APPLICANT Pleach, Gunnar
| APPLICANT: Blau, Astrid
| APPLICANT: Blau, Astrid
| APPLICANT: Clein, Mathieu
| TITLE OF INVENTION: Identification of Herbicidally Active Substances
| TITLE OF INVENTION INVERS: US/10/467, 962B
| CURRENT APPLICATION NUMBER: US/10/466
| PRIOR PILING DATE: 2003-08-14
| NUMBER OF SEQ ID NOS: 109
| SOFTWARE: Patentin Vers: 2.0
| SEQ ID NO 10
| LENGTH: 471
                                                                                                                                                                                                                                                                                                                475 GTGTTATTAAACCCT-------GCGCCAGCATTACGGATTAGAT
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                                                Conservative:
Mismatches:
Indels:
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                  Length:
Matches:
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; ORGANISM: Arabidopsis thaliana
US-10-467-9628-10
              0.000691
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                                                  Percent Similarity:
Best Local Similarity:
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Alignment Scores:
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             471
58
41
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           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                       US-10-049-750-11 (1-921) x US-10-467-962B-10 (1-471)
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             0.0341
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                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Alignment Scores:
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1562 AlaSerThrThrSerSerValLysSerIleSerAspValAlaSerProIleArgSerLeu 1581
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                                                        APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR PLING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SEQ ID NO 1120
SEQ ID NO 1120
LENGTH: 4384
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Matches:
Conservative:
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Sequence 1120, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
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100.50
37.57%
22.25%
6.17%
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US-10-821-234-1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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GCGGGCGATGCCTTTATCGGCTGTTTCGCGCATTACTACGTCCAGAGCGGGGATGTGGGAA 807
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80 IleLeu-----GlnLeuSerSerGluAsnHisValLysAspAlaAlaLeuGluVal
                                   568 ATATTAACCGGTATGCCAGTGGATACCTATGACCATATTCGCGCAGCGGCACGTTCGCTG
                                                                                                       528 GTAGATAAAGGCCTGAACAATATTATTGTCACCATGGGCGAGAAAGGCGCGCTGTGGATG
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                                                                                                                                                                          ACGCGTCACCAGGAAGTCCATGTTCCGGCGTTTAGAGTGAACGCTGTTGATACCAGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CHIRON SpA
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT PILIGN DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR PILIGNED DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMin99, version 1.04
SEQ ID NO 3254
LENGTH: 320
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3254, Application US/10467657; Publication No. US20050260581A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ), ORGANISM: Neisseria gonorrhoeae US-10-467-657-3254
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1679 SerSerProLeuLysSerValValSerProValLysSerArgValAspValIleSerSer 1698
                                                                    .699 AlaLysIleThrMetAlaSerSerLeuSerSerProValLysGlnMetProGlyHisAla 1718
                                                                                                                                         1719 GluvalAlaLeuvalAsnGlySerIleSerProLeuLysTyrAlaSerSerThrLeu 1738
                                                                                                                                                                                             1767 ThraspThrValGluLysValPheSerThrThrThrAlaMetProPheSerProLeuArg 1786
                                                                                                                                                                                                                                                                                                                                                                                                                               1787 SerTyrValSerAlaAlaProSerAlaPheGinSerLeuArgThrProSerAlaSerAla 1806
                                                                                                                                                                              GTACACGGTACTTTTTCTACATACGTCGTATTGATCCCCCAGGATTCGAGATTACGAATG 207
                                                                                                                                                                                                                                                   206 GTGTTGTCGGCAAAAATATCGTCGCCCACT------TTGGTCAACATCAAT 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND FROTEINS
FILE REFERENCE: PU3480U2
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR PILIATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PREENTIN Ver. 2.1
SEQ ID NO 448
LENGTH: 187
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                                                                                                                                                                                                                                                                                                                         161 ACTITIGAATIGAGCITAGCGGCCGCCACGGCCTGGTICGCCCCTITITCCGCCG-----
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Matches:
Conservative:
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Best Local Similarity:
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US-10-793-626-448
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US-10-793-626-448
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                                                                                                                                                                                      85 GCGCCGGCGTTTAAAATCGGCTGCGGGAAAAGGGGCGAACCAGGCCGTGGCGGCCGCT 144
                                                                                                                                                                                                                                                  145 AAGCTC------AATTCAAAAGTATTG---ATGTTGACCAAAGTGGGCGAC 186
                                                                                                                                                                                                                                                                                                                 187 GATATTTTGCCGACAACACCATTCGTAATCTCGAATCCTGGGGGATCAATACGACGTAT 246
                                                                                                                                                                                                                                                                                                                                                                              247 GTAGAAAAGTACCGTGTACCAGCAGCGGCGTAGCGCCGATTTTCGTCAACGCCAACTCC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                           307 AGCAACAGCATTCTGATCATCAAAGGCGCTAACAAGTTTCTCTCGCCGGAAGATATCGAT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----CACGGGATTGAAGTGTTATTAAACCCTGCGCCAGCATTACGGGAATTAGAT 513
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GlyAlaIleProVal------ValGlyProLeuArgArgSerLeuAlaGly 162
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190 TyrAlaAspSerLeuAlaGluAlaThrArgLeuGlyTyrAlaGluAlaAspProThrAla 209
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------GluLeuThrGluAspAlaPheAlaLeuIleGluArgGluAspValAsp 88
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6 AlaProSerPheAsn-----ProGlyLysGlyProGlySerAlaValGlyIleAla
                                                                                                                                                                                                                                                                                                                                                                                                              62 IleSerLyB------ProArgGluGlyValAlaPro-------
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                                                                        Conservative:
Mismatches:
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                                            Length:
Matches:
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                                                           87.50
38.32%
23.36%
5.50%
                                            0.636
                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-467-657-7660
                               Alignment Scores:
Pred. No.:
US-10-858-730-209
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ArgAsnGlnGlnLeuIleArgLeuAspPheGluGluHisProAsnArgGluValLeu--- 136
                                                                                                                                           ------giuglnijerysArgivaTyrArgdiulle 146
                                                                                                                                                                                              185 -----LysGlyAspAspTyrGluLysTyrValGlyAlaThrLeuIleThrProAsnCys 202
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                                              ACCAGCAGCAGCAGCAGCAGCTTTTCGTCAACGCCAACTCCAGCAACAGCATTCTGATC 324
                                                                                                           |||::::::|||
|SerAspMetlleAspTrpAlaLysHisValGlyLysThrValLeuIleAspPro-----
                                                                                                                                                                                                                                                                                                     GCATTACGGGAATTAGATATGTCTTATGCCTGTAAATGCGATTTCTTTGTACCTAATGAA
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SEQUENCE 200, Application US/10858730

SEQUENCE 200 Application US/10858730

SEDICANT: Balley, Richard B.
APPLICANT: Blonquist, Paul
APPLICANT: Driggers, Edward M.
APPLICANT: Driggers, Edward M.
APPLICANT: O'Leary, Jessica
APPLICANT: O'Leary, Jessica
APPLICANT: O'Loole, George
APPLICANT: O'Loole, George
APPLICANT: Trucheart, Joshua
APPLICANT: Walbridge, Michael J.
APPLICANT: Walbridge, Michael J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: METHODS AND
CURRENT APPLICATION NUMBER: US 60/475,000
PRIOR APPLICATION NUMBER: US 60/475,000
PRIOR APPLICATION NUMBER: US 60/551,860
PRIOR APPLICATION NUMBER: US 60/551,860
PRIOR PILING DATE: 2004-06-01
PRIOR PILING DATE: 2004-03-10
NUMBER OF SEC ID NOS: 364
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATACCAGCGCGCGCGATGCCTTTATC-----
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Cys 283
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271 LeuAspLeuGlyIleProLeuThrLeuIleSerGluAlaValPheAlaArgCysValSer 290
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----AATGAAACCGAGCTGGAA 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2530, Application US/10793626
| Sequence 2530, Application US/10793626
| Publication No. US20050258478A1
| GENERAL INFORMATION:
| APPLICANT: KIMMERLY, WILLIAM JOHN
| TITLE OF INVENTION: STAPHYLOCCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
| FILE REFERENCE: PU3480US
| CURRENT APPLICATION NUMBER: US/10/793,626
| CURRENT PILING DATE: 10904-03-04
| PRIOR FILING DATE: 1999-11-09
| NUMBER OF SEQ ID NOS: 4472
| SEQ ID NO 2530
| LENGTH: 186
| LENGTH: 186
                                                                 568 ATATTAACCGGTATGCCAGTGGATACCTAT---GACCATATTCGCGCAGCGGCACGTTCG
                                                                                                                                                     |||:::||| |||:::|||
241 TyriysAspGluGlyGlyGluProLeuAlaGluLysIleLeuAspThrAlaGlyGlnLys
                                                                                                                                                                                                                         733 GTTGAT------ACCAGCGGCGCGCGATGCCTTTATCGCCTGT-----
                                                                                                                                                                                                                                                                                                                                      772 ---TTCGCGCATTACTACGTCCAGAGCGGGGATGTGGAAGCC--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595 TATGACCATATTCGCGCAGCGCACGTTCGCTGGTAGATAAA---GGGCTGAACAATATT
               625 CTGGTAGATAAAGGG-----CTGAACAATATTATTGTCACCATGGCGAGAAA
                                                                                                                                                                                                   GGCGCGCTGTGGATGACGCGTGACCAGGAAGTCCATGTTCCGGCGTTTAGAGTGAACGCT
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US-10-793-626-2530
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                        261 GlyThrGlyLysTrpThr--------
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity:
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| ArgalaTrpGluAlaValLysProIlePheGlnAlaIleAlaAlaLysThrProGlnGly 166
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------AspMetGlnLeuIleCysGluAlaTyrGlnPheMetLysAspGlyLeu 208
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70 IleMetMetWetValArgAlaGlySerValValAspAspPheValGluGlnLeuLeuPro 89
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              APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPREMENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT PILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMin99, version 1.04
SEQ ID NO 7660
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75
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118
120
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Mismatches:
Indels:
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Matches:
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; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7660
 CHIRON SpA
FONTANA Maria Rita
                                                                                                                                                                                                                                                                                                                                          0.901
86.00
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21.07%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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GATATITITICCCGACAACACCATICGIAAICTCGGAATCCIGGGGGATCAAIACGACGIAT 246
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                                                                                                                                                                                                                                                                          307 AGCAACAGCATTCTGATCATCAAAGGCGCTAACAAGTTTCTCTCGCCGGAAGATATCGAT 366
                                                                                                                                                                                                                                                                                                                                                                       367 CGCGCGCGGAAGATTTAAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTTCAGCTT 426
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102 GluValValLeuAlaAlaLeuLysAlaGlyLysSerValValThrAlaAsnLysAlaLeu 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    574 ACCGGTATGCCAGTGGATACCTATGACCATATTCGCGCAGGGGCACGTTCGCTGGTAGAT 633
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| 190 TyrAlaAspSerLeuAlaGluAlaThrArgLeuGlyTyrAlaGluAlaAspProThrAla 209
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------GluLeuThrGluAspAlaPheAlaLeuIleGluArgGluAspValAsp 88
                      463 -----CACGGGATTGAAGTGTTATTAAACCCTGCGCCAGCATTACGGAATTAGAT
--AATTCAAAAGTATTG---ATGTTGACCAAAGTGGGCGAC
                                                                                                                                                                                                                  62 IleSerLys------ProArgGluGlyValAlaPro------
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APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
TITLE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR PILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SEQ ID NOS: 9218
SEQ ID NO 3330
LENGTH: 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       427 GAAACGGTTTATCACGCAATAGAATTTGGCAAGAAA----
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  145 AAGCTC
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| CysThrPheSerAlaVallleThrAlaGluLeuAlaLysGlyArgSerIleLysAspAla 147
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                                              108 AsnGluThrTyrThrPheGluAsnLysArgPheAspThrLysHisThrHisGlyThrGly
                                                                                               754 GATGCCTTTATCGGCTGTTTCGCGCATTACTACGTCCAGAGCGGGGATGTGGAAGCCGCC
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SEQ ID NO 170
LENGTH: 445
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APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Gregor
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: OFFICE STATHWAY PROTEINS
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
TILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148,613
PRIOR PILING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-08
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Conservative:
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Publication No. US20050260707A1
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37.59%
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APPLICANT: Pompejus, Markus
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US-11-055-822-170
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DB:
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SOFTWARE: Seqwin99, version 1.04; SEQ ID NO 2702
LENGTH: 400
                                                        ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2702
NUMBER OF SEQ ID NOS: 9218
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                                                                                                                                                                                                                                                                                                                                                                                           561 GCTGGAAATATTAACCGGTATGCCAGTGGATACCTATGACCATATTCGCGCAGGGGCACG 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                      621 TTCGCTGGTAGAT------AAAGGGCTGAACAATATTATTGTCACCATGGGCGA 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     669 GAAAGGCGCCCTGTGGATGACGCGTGACCAGGAAGTCCATGTTCCGGCGTTTAGAGTGAA 728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2702, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: CHIRON SpA
; APPLICANT: PONTANA Maria Rita
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS;
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS;
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS;
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR PILING DATE: 2001-02-12
                                                          244
51
21
68
63
                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                               US-10-049-750-11 (1-921) x US-10-467-657-3330 (1-244)
                                                                                                                                                                                                                                                                                 102 GlnTyrThrAsnGlyArgArgIleGlnThrGly----
                                                                                                                                                                                             363 CGATCGCGCGCGCAAGATTTAAA------
 , ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3330
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5.22
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Best Local Similarity:
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US-10-467-657-2702
                                            Alignment Scores:
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44 GluPheTrpAlaGluPheArgArgAspLeuLysHisTyrValGlyArgProSerProVal 63
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                                                                                                                                                                                                                                                                               184 AACCCTGCGCCAGCATTACGGAATTAGATATGTCTTAT---GCCTGTAAATGCGAT---
                                                                                                                                                                                                                                                                                                        24 ThrLeulleProAlaLeuLysGluLeuGluGlnAlaTyrAsnGluAlaLysAsnAspPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        555 GTCACCATGGGCGAGAAAGGCGGG----CTGTGGATGACGCGTGACCAGGAAGTCCATGTT
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Mismatches:
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                Length:
Matches:
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              1.64
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                                                        Percent Similarity:
Best Local Similarity:
Alignment Scores:
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                                                                                                Query Match:
DB:
                     .. No. .
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probable carbohydrate kinase STY3989 [imported] - Salmonella enterica subsp. enterica se probable carbohydrate kinase STY3989 [imported] - Salmonella enterica subsp. enterica serovar Typhi 5,Note: this species has also been called Salmonella typhi cjpate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 [S.Accession: AE0963]

R.Parkhill, J.: Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A.; Aluthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova; Reference mumber: AB0502; MUID:21534947; PMID:11677608

A; Residues presidential ary
A; Mesidues 1:7906 cPARA.
A; Residues type: DNA
A; Residues: 1:706 cPARA.
A; Resi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: UNIPARC: UPI00000380F2; GB: AL513382; PIDN: CAD03201.1; PID: 916504832; C; Genetics:
                            ribokinase (import
ribokinase VCA0131
probable ribokinase
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ribokinase (Import
hypothetical prote
ribokinase (EC 2.7
probable ribokinase
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A75599
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AD2421
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T44955
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S40827
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AF2933
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G72752
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A;Gene: STY3989
C;Superfamily: ribokinase
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-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/Cog1_1/USFPTO_spool p/US10049750/runat_23122005_113553_6303/app_query.fasta_1.1742
-Q=/Cog1_2_1/USFPTO_spool p/US10049750/runat_23122005_113553_6303/app_query.fasta_1.1742
-DEV_BETR_CPRYTE_fastan -SUPFTX=n2p.rpr -MINNATCH=0.1 -LOOPCIE=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -ALIGN=15 -MODE=LOCAL
-UNITS=bits -START=1 -END=-1 -MATRIX=S00000000
-USER=US10049750_@CGN 1 1 83 @runat_23122005_113553_6303 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGG_SCORES=0 -MALT -DSPBALCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XCAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                atggatatcgcggttattgg.....atctttcgttgaacgaataa
                         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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T13380
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Ygapop 10.0 , Ygapext
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                                                                                                protein search, using
                                                                                                                                  December 23, 2005,
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seq length: 200000000
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Match
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Database

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Title: Perfect score:

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Scoring table:

probable fructokin probable sugar kin probable carbohydr fructokinase BH185 hypothetical prote

120 20

1570 878 878 550 550 474.5 468.5 468.5 468.5 460.5 450.5

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Result No.

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A;Cross-references: UNIPROT:Q8U6G0; UNIPARC:UPI0000D2715; GB:AE008689; PIDN:AAL45641.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: rbsk
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Matches:
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                                                                                                                         7.41e-69
878.00
76.25$
56.19$
                                                                                   A;Map position: linear chromosome
C;Superfamily: ribokinase
                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                               A; Residues: 1-312 < KUR>
            A;Status: preliminary
A;Molecule type: DNA
 A; Accession: AC3153
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ribofinase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
c;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AG3153
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Kary, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Berr, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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                                           GGCGACGATATTTTGCCGACAACACCATTCGTAATCTCGAATCCTGGGGGATCAATACG
                                                                                    AACTCCAGCAACAGCATTCTGATCATCAAAGGCGCTAACAAGTTTCTCTCGCCGGAAGAT
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Libokinase PA1950 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83403
C;Accession: B83403
C;Accession: B83403
C;Accession: B83403
A;Ederence unuber: A82950; MulD:20437337; PMID:10984043
A;Acference number: A82950; MulD:20437337; PMID:10984043
A;Accession: B83403
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165 ProAlaProAlaAlaAsnLeuAspProGluArgIleArgGlnValThrPheLeuVal 184
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ValLeuValValGlySerLeuAsnMetAspLeuValValArgAlaProArgLeuProArg
                                                                         607 CGCGCAGCGCCACCTTCGCTGGTAGATAAAGGGCTGAACAATATTATTGTCACCATGGGC
205 ValargalaalaargSerLeulleAlaArgGlyIleArgThrVallleValThrLeuGly
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                                                CCTAATGAAACCGAGCTGGAAATATTAACCGGTATGCCAGTGGATACCTATGACCATATT
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C;Superfamily: ribokinase
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Percent Similarity:
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-oft-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: H98134
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Mollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 233-2338, 2001
A;Fitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Retus: preliminary
A;Molccule type: DNA
A;Retus: preliminary
A;Molccule type: DNA
A;Residues: 1-312 < KUR>
A;Residues: 1-312 < KUR>
A;Coss-references: UNIPROT:Q8U6GO; UNIPARC:UPI0000D2715; GB:AE007870; PIDN:AAK88602.1;
C;Genetics:
A;Gene: AGR L. 78
A;Map position: linear chromosome
C;Superfamily: ribokinase
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85 ValValLygValSerGlyLygSerGlyValAlaProllePheValGluGlnSerGly 104
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                                    GTCCAGAGCGGGGATGTGGAAAGCCGCCATGAAAAAAGCCGTCCTCTTTGCCGCTTTCAGC
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Matches:
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76.25%
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Best Local Similarity:
Query Match:
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Pred. No.:
Score:
              787
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LysGlyAsnArgArgAlaPheGluIleAlaArgSerHisGlyValThrThrPheLeuAsn 196
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                                                            ||| ||| ||||||| ::: |||||||:::
|IleValValPheGlySerIleValGlnAspLeuValSerTyrThrAspSerPheProArg
                                                                                                                                                                                                                      ||||:::||| |||:::||| AspMetPheGlyAspSerAsnIleLysAspLeuSerSerAsnGlyValAspThrSerCys
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217 ThrAsnGluAsnGluAlaGluPheIleThrGlyIleAlaGlnAsnAsnValLysAspAla
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C;Specias Caenorhabditis elegans
C;Accession: T20529
R;Reference number: Z19287
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  GTAGAAAAAGTACCGTGTACCAGCAGCGGGGTAGCGCCGATTTTCGTCAACGCCAACTCC
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A;Introns: 19/1; 49/2; 136/1; 221/3; 259/1; 284/3
C;Superfamily: ribokinase
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C;Superfamily: ribokinase
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  Ogud
K.;
                                    Lancet 357, 1225-1240, 2001

A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

A; Reference number: A89758; MUID:21311952; PMID:11418146

A; Reference number: A89759

A; Status: preliminary

A; Molecule type: DNA

A; Cross-references: UNIPROT:Q99WV7; UNIPARC:UPI00000CA992; GB:BA000018; PID:g13700184;

A; Experimental source: strain N315

C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: ribokinase
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
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Libokinase (EC 2.7.1.15) - Bacillus subtilis

Cispecies: Bacillus subtilis

Cidaceslon: Débéso, 140465; 842711

Rikunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; C.

A; Enlich, B. D.; Emmerson, P. T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Ajuthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, S.; Envocot, C.; Fruschi, C.V.; Caldwell, B.; Capuano, V.; Garter, N.M.; Muture 390, 249-256, 1997

Ajuthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, S.; Envoceter, P.; Knoingstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, N.; Aluthors: Lauber, J.; Lazarevic, V.; Ede, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueelly, M.; M.; Ogawa, K.; Ogiwara, A.; Tanaka, T.; Tarpstra, P.; Sadio, Y.; Sako, T.; Sakowska, A.; Sarou, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Setiguchi, J.; Sekowska, A.; Sarou, A; Authors: Schleich, S.; Zunstein, B.; Yose, M.; Yasumoto, K.; Wacaserecenesu Unipror; Etrain 168

A; Attle: R.; Analysis of a ribose transport operon from Bacillus subtilis.

A; Racerone number: Idd62; Mulpagoto, V.; Pulpagoto, V.; Yasumoto
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A;Molecule type: DNA
A;Residues: 1-283,'DKK' <RES>
A;Residues: 1-283,'DKK' <RES>
Cross-references: UNIPARC:UPI00016E934; EMBL:Z25798; NID:g397493; PIDN:CAA81049.1; PI
C;Comment: This enzyme catalyzes the phosphorylation of ribose to ribose 5-phosphate, the C;Genetics:
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AB0952
ribokinase [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0952
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T. T; Connerton, P; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
                                        183
                                                                                 GACGATATTTTGCCGACAACACCATTCGTAATCTCGAATCCTGGGGGATCAATACGACG 243
                                                                                                                                                                   363
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LeuAsnAlaLeuGluGlnIleGluLysValAspMetValLeuIleGlnGlnGluIlePro 141
                                                                                                                                                                                                                                                               AsnProAlaProAla---ArgProLeuLysGlnGluThrIleAspHisAlaThrTyrLeu 180
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TyrMetGluProValThrHisThrGluSerGlyThrAlaHisIle---ValLeuAlaGlu 101
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           AAAGAAGGGGAAACTCTGGAAGCGCCGGCGTTTAAAATCGGCTGCGGCGGAAAAGGGGCG
                                         AACCAGGCCGTGGCGCCGCTAAAGCTCAAAAGTATTGATGTTGATCAAAGTGGGC
                                                                                                                                                                   364 GATCGCGCGCGCAACATTTAAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTTCAG
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A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0952
A;Status: preliminary
A;Aclassion: DNA
A;Residues: 1-309 <PAR>
A;Cross-references: UNIPARC:UPI000005A66C; GB:AL513382; PIDN:CAD03110.1; PID:g16504746; C;Genetics:
A;Genetics:
C;Genetics:
C;Superfamily: ribokinase
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66 AspAspAspIleGlyAspSerIleArgLysGlnLeuValSerAspArgIleAspIleAla
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Matches:
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52.16%
37.54%
29.47%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Tibokinase (EC 2.7.1.15) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Date: 02-NOV-2001 #sequence_revision 02-NOV-2001 #text_change 09-Jul-2004
C;Accession: A10001
C;Accession: A10001
C;Accession: A10001
G;Accession: A10001
G;Accession: A10001
A; Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T; Cronin, A.; Davies, R.M.; Davies, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A;Molecule type: DNA
A;Residues: 1-308 «KUR»
A;Cross-references: UNIPROT:Q8ZJS8; UNIPARC:UPI0000DCD63; GB:AL590842; PIDN:CAC88875.1
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                                                                                                                                                                                                                                                                                                 637 GGGCTGAACAAT---ATTATTGTCACCATGGGCGAGAAAGGCGCGCTGTGGATGACGCGT 693
221 GlyValargLysAlaValileIleThrLeuGlySerGlnGlyAlaTyrTyrLysSerAla 240
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            GCCTGTAAATGCGATTTCTTTGTACCTAATGAAACCGAGCTGGAAATATTAACCGGTATG
                                                                                                                                     694 GACCAGGAA---GICCAIGITCCGGCGITTAGAGIGAACGCTGTIGAIACCAGCGGCGCG
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C;Superfamily: ribokinase
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Dete: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Dete: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: 139594
R;Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
submitted to the EMBL Data Library, May 1998
A;Reference number: 221866
A;Accession: T39594
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Retus: preliminary; translated from GB/EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 TIGATGTTGACCAAAGTGGGCGACGATATTTTGCCGACAACACCCATTCGTAATCTCGAA 222
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LysAspGlyvalAsnValAspAsnValLysLysIleGluAsnLysSerThrGlyValAla 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 TCCTGGGGGATCAATACGACGTATGTAGAAAAAGTACCGTGTACCAGCAGCGGCGTAGCG 282
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                                                                                               AGCGTCACCGGGAAAGGCACCCAATCCTCTTATCCAAGCATTGAGCAATTTAATGAGTAT
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124 AlaAlaPheGluGlnGluLeuAlaAlaSerAspValValLeuLeuGlnLeuGlullePro 143
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                                                                                                                                                                                                             GACGATATTTTTGCCGACAACACCATTCGTAATCTCGAATCCTGGGGGATCAATACGACG
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|LeuGluThrValAlaTyrValLeuGluPheCysAlaLysHisHisValThrThrValLeu
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201 LeuArg------GlnLysLeuIleMetThrLys
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                                                       3.5e-32
460.00
55.81%
37.54%
28.93%
               C, Superfamily: ribokinase
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Best Local Similarity:
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H84115
ribokinase rbsK [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: H84115
R;Takami, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A89650; MuID:20512582; PMID:11058132
A;Accession: H84115
A;Accession: H84115
A;Accession: H84115
A;Accession: H84115
A;Reduce: L04
A;Molecule type: DNA
A;Residues: 1-294 <STO>
A;Cross-references: UNIPROT:Q9K6K1; UNIPARC:UPI00001333E4; GB:AP001519; GB:BA000004; NIC
A;Experimental source: strain C-125
C;Genetics:
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86 IleGluAlaIleLysGlyAlaThrThrGlyValAlaLeuIlePheValAsnSerAspGly 105
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AspThrVallleAlaAlaAlaAlaYsLeuAlaLysGlnHisGlnThrGlnVallleLeuAsn 165
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LeuLeuGluGlyGlnSerMetABpValAlaValArgPheAlaHisAlaAlaAlaIle 283
                                                                                                                       GTAGAAAAAGTACCGTGTACCAGCAGCGGCGTAGCGCCGATTTTCGTCAACGCCAACTCC 306
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                    GATATTTTGCCGACAACACCATTCGTAATCTCGAATCCTGGGGGATCAATACGACGTAT
                                                                             CGCGCGGGGAAGATTTAAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTTCAGCTT
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Length: Matches: Conservative: Mismatches: Indels:

44

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483

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200 663 209 248 843 AGCGTCACCGGGAAAGGCACCCAATCCTTATCCAAGCATTGAGCAATTTAATGAGTAT 903 

269

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ribokinase (b. 4., 1.1.). - naemoppillus intiuenizae (Bergin RG NWZO)
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: B64073
R;Fleischmann, R.D.; Admas, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. R;Pleischmann, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidmann, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Fuhrmann, J.L.; Geoghagen, N.S.M. Scotnec 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: B64073
A;Accession: B64073
A;Residues nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-306 < TIGR>
A;Cross-references: UNIPROF:P44331; UNIPARC:UP100001333E5; GB:U32732; GB:L42023; NID:91EC;Keywords: phosphotransferase; ribose metabolism
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LeuThrValLeuGlySerIleAsnAlaAspHisValIleSerValProTyrPheThrLys
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544 GTACCTAATGAAACCGAGCTGGAAATATTAACCGGTATGCCA---GTGGATACCTATGAC
                                                                                                              ATCGGCTGTTTCGCGCATTACTACGTCCAG-----AGCGGGGATGTGGAAGCCGCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                         817 AAAAAAGCCGTCCTCTTTGCCGCTTTCAGCGTCACCGGGAAAGGCACCCCAATCCTCTTAT
                                                                                     CATATTCGCGCAGCGGCACGTTCGCTGGTAGATAAAGGGCTGAACAATATTATTGTCACC
                                                                                                                                                                           661 ATGGGCGAGAAAGGCGCGCTGTGGATGACGCGTGACCAGGAA------GTCCATGTT
                                                                                                                                                                                                       B64073
ribokinase (EC 2.7.1.15) - Haemophilus influenzae (strain Rd KW20)
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A;Map position: 84 min
C;Complex: homodimer (in solution); [validated, MUID:98046763]
C;Punction: EC 2.7.1.15 [validated, MUID:86224052]; catalyzes the phosphorylation of
C;Superfamily: ribokinase
C;Keywords: ATP; phosphotransferase; ribose metabolism
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KIECRB
ribokinase (EC 2.7.1.15) [validated] - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Decies: Bacherichia coli
C;Decies: Bacherichia coli
C;Decies: Bacherichia coli
C;Decies: 11-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession. 245065, A65179
R;HOpe, J.N.; Bell, AW: Hermodson, M.A.; Groarke, J.M.
J. Biol. Chem. 261, 7663-7668, 1986
A;Title: Ribokinase from Escherichia coli K12. Nucleotide sequence and overexpression
A;Reference number: A26305; MUD:86224052; PMID:3011794
A;Residues: 1-309 *HOP>
A;Residues: 1-309 *HOP>
A;Cross-references: UNIPROT:P05054; UNIPARC:UP1000003EB7F; GB:M13169; GB:M13517; NID:9
A;Escheriental source: strain K12
A;Residues: D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1467, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A65179
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Mocacule type: DNA
A;Residues: 1-309 *BLAT>
A;Cross-references: UNIPARC:UP1000003EB7F; GB:U00096; NID:g1790188; PIDN:
C;Genetics:
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                                    GTAGAAAAAGTACCGTGTACCAGCAGCGGCGTAGCGCCGATTTTCGTCAACGCCAACTCC 306
                                                         :::
IleAsnThrValSerGlnGluMetThrGlyMetAlaPheIleGlnValAlaLysSerSer 104
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ProAlaProAla---GlnIleLeuSerAspGluLeuLeuSerLeuIleAspIleIleThr 183
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AspSerIleGlyLysThrMetLysAsnAlaPheAlaGlnGluGlyIleAspThrThrHis 84
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727 AACGCTGTTGATACCAGCGGGGGGGGGGTGCCTTTATCGGCTGTTTCGCGCATTACTAC 786
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Enterobacteriaceae; Salmonella.
NCBI_TaxID=602;
                                       081149 | 0014477 | 0014477 | 0014477 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133 | 0019133
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative sugar kinase (EC 2.7.1.15).
OrderedLocusNames=STM3793;
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QBNYG7_S
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008316_P
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008RD45_I
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(c) 1993 - 2005 Compugen Ltd
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Q4LSVS_9BURK
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Q63M06_BURPS
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WICHEQUIDE SEQUENCE.

WEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;

WEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;

WEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;

Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

Croin A., Davies R.M., Dowd L., White N., Farrar J.,

Roull T., Hamlin N., Haque A., Hier S., O'Gaora P., Parry C.,

Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

A Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,

Whitehead S., Barrell B.G.;

Whitehead S., Barrell B.G.;

Whitehead S., Barrell B.G.;

Whitehead S., Barrell B.G.;

Complete genome sequence of a multiple drug resistant Salmonella

Therefore a serovar Typhi CT18.";

Complete genome sequence of a multiple drug resistant Salmonella

Therefore A.AO71218.1; -; Genomic_DNA.

EMBL; AE016846; AAO71218.1; -; Genomic_DNA.

EMBL; AL627280; CAD03201.1; -; Genomic_DNA.

EMBL; AL627280; CAD03201.1; -; Genomic_DNA.

EMBL; AL627280; CAD03201.1; -; Genomic_DNA.

EMBL; PRO16301; F: Kinase activity; IEA.

GO; GO:0006947; F: Transferase activity; IEA.

GO; GO:0006014; P: Pribose metabolism; IEA.

GO; GO:0006014; PERD: Tribose metabolism; IEA.

RO; GO:0006014; PERD: Tribose metabolism; IEA.

RO; GO:0006014; PERD: Tribose metabolism; IEA.

RINTE: PRO02139; RIBOKINASE.

REPURD: PRO01837; PERD: D'IDNINASE.
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MEDLINE=22531367; PubMed=12644504;
DOI=10.1128/JB.185.7.2330-2337.2003;
Dong W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
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Enterobacteriaceae; Salmonella.
NCBI_TaxID=601;
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Complete protecome; Kinase.
SEQUENCE 306 Aa; 33229 MW; 142A0289E2D1B953 CRC64;
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QBXGWS_SALTI PRELIMINARY; PRT; 306 AA.
QBXGWS; Q7ALZ9;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
O1-MAR-2005 (TrEMBLrel. 30, Last annotation update)
Putative carbohydrate kinase.
OrderedLocusNames=STY3989, t3725;
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OSFURI; OSFURI; 306 AA.
OSFURI; OSFURICAL 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Putative carbohydrate kinase.
OrderediccusNames=SPA3643;
Salwonella paratyphi-a.
Salwonella paratyphi-a.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobs
Enterobacteriaceae; Salmonella.
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PubMed=15531882; DOI=10.1038/ng1470;

McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,

Dorwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,

A Harkins C.R., Wang C., Nayven C., Berghoff A., Elliott G.,

McMlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,

Leonard S., Sun H., Pulton L., Nash W., Minnx P.,

Delehaunty K., Pronick C., Magrini V., Nhan M., Warren W., Florea L.,

Spieth J., Wilson R.K.;

"Comparison of genome degradation in Paratyphi A and Typhi, human-
restricted serovars of Salmonella enterica that cause typhoid.",

IN at. Genet. 36:1268-1274(2004).

EMBL; CP0000056; AAV79437.1; -Genomic_DNA.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0016304; F:ribokinase activity; IEA.

GO; GO:0006975; P:carbokydrate metabolism; IEA.

GO; GO:0006917; P:D-ribose metabolism; IEA.

McPrepro; IPR01187; Dribokinase.

EnterPro; IPR01187; Dribokinase.

EnterPro; IPR01187; Pika Fegion.

EnterPro; IPR012139; Ribokinase.
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PRINTS; PR00990; RIBOKINASE.
TIGRAFAMB; TIGR02152; Dribokin_bact; 1.
COMPLETE proteome; Kinase.
SEQUENCE 306 AA; 33229 MW; 142A028952D1B953 CRC64;
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TTCAGCGTCACCGGGAAGGCACCCAATCCTTATCCAAGCATTGAGCAATTTAATGAG
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                                                                                                     AACTCCAGCAACAGCATTCTGATCATCAAAGGCGCTAACAAGTTTCTCTCGCCGGAAGAT
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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PubMed=15385522; DOI=10.1128/IAI.72.10.6151-6156.2004;
Bernier-Febreau C., Du Merle L., Turlin E., Labas V., Ordonez J.,
Gilles A.M., Le Bouguenec C.;
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Q67FX7;
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                                CATATTCGCGCAGGCACGTTCGCTGGTAGATAAAGGGCTGAACAATATTATTGTCACC
                                           ATGGGCGAGAAAGGCGCGCGCGTGACGCGTGACCAGGAAGTCCATGTTCCGGCGTTT
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Pubmed=15781495;
Chiu C.-Hu S., Bao Q., Yu J., Chou Y.-Y.,
Wang H.-S., Lee Y.-S.;
Wang H.-S., Lee Y.-S.;
Highly invasive and resistant zoonotic pathogen.";
Nucleic Acids Res. 33.1.690-1698 (2005).
EMBL; AB017220; AAX67619-1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                             33 SALCH

57143 SALCH PRELIMINARY; PRT; 306 AA.

657143 SALCH PRELIMINARY;
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Putative sugar Kinase, ribokinase family.
Name=rbsK; OrderedLocusNames=SC3713;
Salmonella cholerae-suis (Salmonella enterica).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriais Gammaproteobacteria; Enterobacteriais (Salmonella).

Enterobacteriaceae; Salmonella.
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Sacterial Collidarian Collidarian Sactorial Sactorial Sactorial Sacterial Proteobacteria; Gammaproteobacteria; Bnterobacteriales; Bacteria; Broteobacteriaceae; Escherichia.

DE Enterobacteriaceae; Escherichia.

NCBI_TAXID=217992;

(1)

RDI_LIDATIDE SEQUENCE.

NCBI_LINE=22388234; PubMed=12471157; DOI=10.1073/pnas.25529799;

RASACO D., Bucklas B.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Backlas B.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Backlas B.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Rasko D.J., Stroud S., Schwartz D.C., Perna N.T., Mayhew G.F., Rose D.J., Solwartz D.C., Perna N.T., Mayhew G.F., Rose D.J., Solwartz D.C., Perna N.T., Mayhew G.F., Rose D.J., Solwartz Complete genome sequence of uropathogenic Escherichia coli.;

RE Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.;

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

BRID: Abolf56; AAN78819.1; -; Genomic_DNA.

RSSP; POSO54; IRKD.

GO; GO:0006747; F:ribokinase activity; IEA.

BR GO; GO:000677; F:ribokinase activity; IEA.

RO; GO:000671; P:Dribose metabolism; IEA.

RO; GO:000671; PRO1187; Pibbkinase.

RIMERPRO: IPRO1187; Pibbkinase.

RIMERPRO: IPRO1187; Pibbkinase.

RIMERPRO: PRO0294; PERB; Ribokinase.
                                                                                                   TyrTyrValGlnSerGlyAspValGluAlaAlaLeuLysLysAlaAlaAlaAlaAla
                           201 HislleArgLeuAlaAlaArgSerLeuValAspLysGlyLeuAsnAsnIleIleValThr
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TIGRFAMB; TIGR02152; D_ribokin_bact; 1.
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Q8FKR4;
Q1-MAR-2003 (TrEMBLrel, 23, Ca
Q1-MAR-2003 (TrEMBLrel, 23, La
Q1-OCT-2003 (TrEMBLrel, 25, La
Putative ribokinase.
OrderedLocusNames-c0331;
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USE OI DEOXYTIDOSE by Intestinal and Extraintestinal Pathogenic Bscherichia coli Strains: a Metabolic Adaptation Involved in Competitiveness.";
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                                                                                            Infect. Immun. 72:6151-6156(2004).

EMBL; AY298765; AAQ75098.1; -; Genomic_DNA.
EMBL; AY299315; AAQ83788.1; -; Genomic_DNA.
EMBL; AY299316; AAQ83788.1; -; Genomic_DNA.
EMBL; AY299316; AAQ83788.1; -; Genomic_DNA.
GO; GO:0016301; F:Kinase activity; IEA.
GO; GO:0016740; F:Linokinase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR011877; D ribokin bact.
InterPro; IPR011611; PfkB region.
InterPro; IPR02139; Ribokinase.
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Gaps:
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TIGRFAMB; TIGR02152; D_ribokin_bact; 1.
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RT Uropathogenic Escherichia coli Strain 536."; Infect. Immun. 7:5993-6001(2004).

BREMBI, AJ617685; CAR85173.1: -; Genomic DNA.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:001647; F:ribokinase activity; IEA.

GO; GO:0016740; F:ribokinase activity; IEA.

GO; GO:0016740; F:ribokinase activity; IEA.

GO; GO:001614; P:D-ribose metabolism; IEA.

R InterPro: IPRO11611; PřRB región.

R InterPro: IPRO11611; PřRB región.

R InterPro: IPRO2139; Ribokinase.

R PREM: PRO0244; PřRB; I.
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TIGREAMS; TICR02152; D_ribokin_bact; 1.
Hypothetical protein.
SEQUENCE 315 AA; 34327 MW; 8A9721EB9
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562;
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Q70712 ECOLI
D Q70712 ECOLI PRELIMINARY; PRT; 315 AA.
AC Q70712.
DT 05-JUL-2004 (TrEMBLrel, 27, Created)
DT 05-JUL-2004 (TrEMBLrel, 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel, 27, Last annotation update)
DT 05-JUL-2004 (TrEMBLrel, 27, Last annotation update)
DF Hypothetical protein.
OS Escherichia coli.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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MEDLINE-21101044; PubMed=11159989; DOI=10.1128/IAI.69.2.937-948.2001;
Lalioui L., Le Bouguenec C.C.;
Lafa-8 Gene cluster is carried by a pathogenicity island inserted into the tRNA(Phe) of human and bovine pathogenic Escherichia coliminated the tRNA(Phe) of human and bovine pathogenic Escherichia coliminated to the tRNA(Phe) of human and bovine pathogenic Escherichia coliminated the tRNA(Phe) of human and bovine pathogenic Escherichia coliminated the tRNA(Phe) of human and bovine pathogenic Escherichia coliminated the tRNA(Phe) of human and bovine pathogenic Escherichia coliminated the transferase activity; IEA.

GO: GO:0016301; F:kinase activity; IEA.

RO: GO:0016301; F:kinase activity; IEA.

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                         CATATTCGCGCACGCACGTTCGCTGGTAGATAAAGGGCTGAACAATATTATTGTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bscherichia coli.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Escherichia.
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TIGRRAMS; TIGRO2152; D_ribokin_bact; 1.
Hypothetical protein.
SEQUENCE 314 AA; 34415 MW; 2D5F7342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 PheLeuThrLeuAsnGlu 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATCTTTCGTTGAACGAA 918
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90.28%
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                                                                                                                             GGCGACGATATTTTGCCGACAACACCATTCGTAATCTCGAATCCTGGGGGATCAATACG
                                                                                                                                          241 ACGIATGIAGAAAAAGIACCGTGIACCAGCAGCGGCGIAGCGCCGATTITCGICAACGCC
                                                                                                                                                                                       AACTCCAGCAACAGCATTCTGATCATCAAAGGCGCTAACAAGTTTCTCTCGCCGGAAGAT
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                                              30 ProLysGluGlyGluThrLeuGluAlaProAlaPheLysIleGlyCysGlyGlyLysGly
                                                                                            361 ATCGATCGCGCGCGCAAGATTTAAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTT
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ID QTMP36 VIBVY PRELIMINARY;

AC QTMP36 VIBVY (TEMBLE). 20

DT 01-MAR-2004 (TEMBLE). 20
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243
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284 SerValThrGluLysGlyThrGlnPheSerTyrProSer1leGluGlnPheGluGluPhe 303
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                                                                                                                                                                                                                                                                                            607 CGCGCAGCGCCACGTTCGCTGGTAGATAAAGGGCTGAACAATATTATTGTCACCATGGGC
                                                                                                                                                                                              667 GAGAAAGGCGCGCTGTGGATGACGCGTGAC---CAGGAAGTCCATGTTCCGGCGTTTAGA
                                                                          CCTAATGAAACCGAGCTGGAAATATTAACCGGTATGCCAGTGGATACCTATGACCATATT
                                                                                                     GTGAACGCTGTTGATACCAGCGGCGCGCGATGCCTTTATCGGCTGTTTCGCGCATTAC
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STRAIN-LSV54 / DSM 12343;
PubMed=15305914; DDI=10.1111/j.1462-2920.2004.00665.x;
PubMed=15305914; DDI=10.1111/j.1462-2920.2004.00665.x;
Rabus R., Ruepp A., Frickey T., Rattel T., Fartmann B., Stark M., Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K., Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R. Klenk H.-P., Le namilanda navchrophila, a sulfate-reducing bact.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desulfotalea psychrophila.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
Desulfobulbaceae; Desulfotalea.
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In the genome of Desulfotalea psychrophila, a sulfate
from permanently cold Arctic sediments.";

Environ. Microbiol. 6.887-902 (2004).

R EMBL, CR52870; CAG35703.1; -; Genomic_DNA.

R GO; GO:0016301; F:kinase activity; IEA.

R GO; GO:000647; F:ribokinase activity; IEA.

R GO; GO:0006747; F:ribokinase activity; IEA.

R GO; GO:0006775; P:carbohydrate metabolism; IEA.

R GO; GO:0006975; P:carbohydrate metabolism; IEA.

R InterPro; IPR011877; D:ribokin_bact.

R InterPro; IPR011877; D:ribokin_bact.

R InterPro; IRR011877; D:ribokin_bact.

R InterPro; IRR011877; D:ribokin_bact.

R InterPro; IRR012139; Ribokinase.

R PRINTS; PR00390; RIBOKINASE.

R TGRFAMs; TGREAMS; Tibokin_bact; 1.

R Complete proceome; Kinase.

R Complete proceome; Kinase.
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928.00
74.92%
61.20%
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OrderedLocusNames=DP1974;
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                                                                                                                                                                                                                                                                        T.-L.,
                                                                                                                                                                                                                         PubMed=14656965; DOI=10.1101/gr.1295503; Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C., Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.; "Comparative genome analysis of Vibrio vulnificus, a marine
                                            OrderedLocusNames=VV0528;
Vibrio vulnificus (strain YJ016).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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218
42
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         annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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HSSP; P05064; IGQT.
GO; GO:0016301; F:kinase activity, IEA.
GO; GO:0004147; F:ribokinase activity, IEA.
GO; GO:0066014; P:D-ribose metabolism; IEA.
InterPro; IPR011877; D_ribokin_bact.
InterPro; IPR011817; D_ribokin_bact.
InterPro; IPR012139; Ribokinase.
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TIGRPAMS; TIGROS152; D. TiDokin_bact; 1.
Complete proteome; Kinase.
SEQUENCE 309 AA; 33507 MW; EBBBACF6
                                                                                                                                                                                                                                                                                                                                                pathogen.";
Genome Res. 13:2577-2587(2003)
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1137.50
86.67%
72.67%
71.54%
            01-MAR-2004 (TrEMBLrel, 26,
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Percent Similarity:
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                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                     Sugar kinase.
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247 LysAlalysAspThrSerGlyAlaGlyAspAlaPheIleGlyCysPheAlalysHisTyr 266
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04LSV9;
13.SEP-2005 (TrEMBLrel. 31, Created)
13.SEP-2005 (TrEMBLrel. 31, Last sequence update)
13.SEP-2005 (TrEMBLrel. 31, Last annotation update)
Carbohydrate kinase, PfkB.
Carbohydrates=Deen244DRAFT, 3825;
Burkholderia cenocepacia H12424.
                   (1-309)
                   Q6ALS2_DESPS
                   US-10-049-750-11 (1-921) x
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EMBL/ AAHL01000019; EAM19121.1; -; Genomic_DNA.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiale:
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex
NCBI_TaxID=331272;
                                                                         NUCLEOTIDE SEQUENCE.
STRAIN=H12424;
STRAIN=H12424;
STRAIN=H12434;
SOB JOINT Genome Institute (JGI-PGF);
COPELAND A., Lucas S., Lapidus A., Barry K., Detter C., G
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia"
                                                                                                                                                                                                                                                                      Larimer F., Land M.; *Annotation of the draft genome assembly of Burkholderia H12424."; OUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                       HI2424.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
STRAIN=H12424;
US DOE Joint Genome Institute (JGI-ORNL);
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75.33%
61.00%
58.11%
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Best Local Similarity:
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726
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DOE Joint Genome Institute;
DOE Joint Genome Institute;
Chain P., Larimer F., Disartolo G., Copeland A., Lykidis A., Trong S., Nolan M., Goltsman E., Thiel J., Malfatti S., Lapidus A., Detter J.C., Land M., Richardson P.M., Kyrpides N.C., Ivanova N.;
Comparison of two complete genome sequences of Pseudomonas syringae pv. syringae B728a and pv. tomato DC3000.";
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).
                                                                ThrargAlaAlaGluAlaLeuValAlaArgGlyLeuLy8Hi8ValLeuValThrLeuGly
                                                                                                                                                                                                                           CCTAATGAAACCGAGCTGGAAATATTAACCGGTATGCCAGTGGATACCTATGACCATATT
               CGCGCAGCGCCACGTTCGCTGGTAGATAAAGGGCTGAACAATATTATTGTCACCATGGGC
                                                                                                      GAGAAAGGCGCCCCCTGTGGATGACGCGTGACCAGGAAGTCCATGTTCCGGCGTTTAGAGTG
                                                                                                                       |||:::||| ::::::|||| SerAsngAspGlyValHisHisValProGlyValProVal
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Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=205918;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Carbohydrack kinase, PfkB.
ORFNames=P8yr 4487;
Pseudomonas syringae pv. syringae B728a.
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Feil H., Feil W.S., Lindow S.E.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ
SUBEL; CP000075; AAX39517.1; -; Genomic_DNA.
GO; GO:0016301; F:kinase activity; IEA.
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Submitted (MAY-2005)
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Query Match:
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                                                                    204 AlaGlnAlaAlaArgGlnLeuValAlaLeuGlyValArgHisValIleValThrLeuGly
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|GluGlnGlyAlaLeuTyrValGlyAlaGluGlyGluTrpGlnValProGlyValLy8Val
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                                                                                                                                                                                         GATATTTTGCCGACAACACCATTCGTAATCTCGAATCCTGGGGGATCAATACGACGTAT
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ProAsnGluSerGluLeuAlaLeuIleSerGlyGlnProValThrCysAlaGluGluAla
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OrdereddocusNames=BPSS0853;
Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
NCBI_TaxID=28450;
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
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CCTGCGCCAGCATTACGGGAATTAGATATGTCTTATGCCTGTAAATGCGATTTCTTTGTA
                              CCTAATGAAACCGAGCTGGAAATATTAACCGGTATGCCAGTGGATACCTATGACCATATT
                                                                                                                                                   CGCGCAGCGCACGTTCGCTGGTAGATAAAGGGCTGAACAATATTATTGTCACCATGGGC
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MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
MOOL D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Chora V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Lim, J.J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Nester E.W.;
Nester E.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WUCLEOTIDE SEQUENCE.
MUCLEOTIDE SEQUENCE.
MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin I.
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Gielo C., Slater S.;
Genome sequence of the plant pathogen and biotechnology agent
Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUGGG; Q7CW10; 01-JUN-2002 (TrEWBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 13-SEP-2005 (TrEMBLrel. 21, Last sanotation update) Ribokinase (AGR L 78p). Name-Erbsk; OrderediocusNames-AGR L 78, Atu4847; Agrobacterium tumefaciens (strain G58 / ATCC 33970). Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium.
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EMBL; AE008201; AAK88602.1; -; Genomic_DNA.
PIR; AC3153; AC3153.
PIR; H98134; H98134.
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QBUGGO; Q7CW10;
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                                                       STRAINELSEATY,

C. STRAINELSEATY,

D. C. Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,

Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,

A tkine T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,

Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,

Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,

A Chillingworth T., Cronin A., Crossett B., Davis P., Deshazer D.,

Reith K.E., Maddison M., Moule S., Price C., Quail M.A.,

Reith K.E., Maddison M., Moule S., Price C., Quail M.A.,

Rabbinowitesch B., Rutherford K., Sanders M., Slumnonds M.,

Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,

Mitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;

Micholderia pseudomallei";

Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).

EMBL, BS71966; CAHSS16.1; -, Genomic DNA.

GO; GO:0006704; P:ribokinase activity; IEA.

GO; GO:000671; P:ribokinase activity; IEA.

GO; GO:0006014; P:D-ribose metabolism; IEA.

R DG:0000694; P:ribokinase activity; IEA.

R DG:0000694; P:ribokinase.

R InterPro; IPR01187; D:ribokinase.

R Pfam; PF00294 PfkEA.

R Pfam; PF00294 PfkEA.
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TIGRFAMS; TIGR02152; D_ribokin_bact; 1.
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168
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Matches:
Conservative:
Mismatches:
Indels:
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             GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0004747; F:ribokinase activity; IEA.
GO; GO:0006014; P:D-ribose metabolism; IEA.
InterPro; IPR011877; D_ribokin_bact.
InterPro; IPR011611; PfkB region.
Pfam; PP002139; Ribokinase.
Pfam; PP002194; PfkB; I.
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                                                                                                                             PRINTS; PRO0990; RIBOKINASE.
TIGREAMS; TIGR02152; D ribokin_bact; 1.
Complete proteome; Kinase.
SEQUENCE 312 AA; 33094 WW; D2A070A35
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878.00
76.25%
56.19%
55.22%
 HSSP; P05054; 1RKD
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STRAIN-EXPAINING SEQUENCE.

The complete genome sequence of Propionibacterium acnes, a commensal of human skin.

The complete genome sequence of Propionibacterium acnes, a commensal of human skin.

Science 305:671-673 (2004).

EMBL; AE017283; AAT82961.1; -; Genomic_DNA.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0016301; F:ribokinase activity; IEA.

GO; GO:001640; F:rribokinase activity; IEA.

RO; GO:001641; F:ribokinase activity; IEA.

RO; GO:001641; F:ribokinase activity; IEA.

RO; GO:001611; F:Ribokin bact.

RICEPPO; IPR011817; D Libokin bact.

RICEPPO; IPR01181; FKB region.

RICEPPO; IPR01181; FKB region.

RICEPPO; IPR01181; FKB region.
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245 ThrProArgAspThrThrGlyAlaGlyAspAlaPheIleGlySerPheAlaArgPheTyr 264
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                                                                                                                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Propionibacterineae; Propionibacteriaceae; Propionibacterium.
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Sugar kinase, ribokinase family (EC 2.7.1.15).
OrderedLocusNames=PPA1211;
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Matches:
Conservative:
Mismatches:
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TIGRPAMs; TIGR02152; D.ribokin bact; 1.
Complete proteome, Kinase; Transferase.
SEQUENCE 304 AA; 32266 MW; 3C03C7FASFAE2080
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361 ATCGATCGCGCGGGAAGATTTAAAAAATGCCAGCTTATTGTTCTGCAACTGGAAGTT 420
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120 ValGluGlyAlaArgGlnAspIleAlaThrCysLysLeuIleMetLeuGlnLeuGluIle 139
                                                                                                                            781 TACTACGTCCAGAGCGGGGATGTGGAAGCCGCCATGAAAAAGCCGTCCTCTTTGCCGCT 840
                         301 AACTCCAGCAACAGCATTCTGATCATCAAAGGCGCTAACAAGTTTCTCTCGCCGGAAGAT 360
                                    ATGGGCGAGAAAAGGCGCCTGTGGATGACGCGTGACCAGGAAGTCCATGTTCCGGCGTTT 720
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ABJ04044
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(INSP ) INST PASTEUR.
(PHAR-) PHARMA-WALDHOF_GMBH & CO KG.
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Marliere P, Pochet S;
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                                          RESULT
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-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/CgnZ_1/USFPTO spool_p/US10049750/runat_23122005_I13551_6285/app_query.fasta_1.1742
-Q=/CgnZ_1/USFPTO spool_p/US10049750/runat_23122005_I13551_6285/app_query.fasta_1.1742
-DEV_ALIGNS_200 -TRN_200R=pct -TRN_ALN_20.rag -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -ALIGN=15 -MODE=LOCAL
-OUTHERSENCE -TRN_EXCORE=pct -TRN_MAX=100 -TRN_ENS=200000000
-USER=US10049750_@CGN_1 1 476 @runat_23122005_I13551_6285 -NCFU=6 -ICFU=3
-NO_WMAP -LARREQUERY -NGS_CSCRES=0 -MALT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THERAD=1 -XCAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
114 T. ..
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                                                                                                                                                                                                                                                gtatactaaatgccaaaaaa..........acgaaggtgccgtatactaa 483
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                                                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                      - protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                           2443163 seqs, 439378781 residues
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Kgapop 10.0 , Kgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Sequence 157 AA;
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                                                                    The present sequence represents a nucleoside 2-deoxyribosyltransferase enzyme. This enzyme is involved in the biosynthesis of deoxyribonucleosides, and is used in the method of the invention. The specification describes a method for the in vitro enzymatic synthesis of deoxyribonucleosides. The method comprises reacting deoxyribose 1-phosphate and a nucleobase to form a deoxyribonucleoside and an inorganic phosphate. Bnzymes which may be used in the method of the invention include thymidine phosphorylase, purine nucleoside phosphorylase, purine nucleoside phosphorylase, plosphopentose aldolase, fructose 1,6-diphosphate aldolase, deoxyribokinase, and nucleoside 2-deoxyribosyltransferase
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               enzymatic synthesis of deoxyribonucleosides comprises reacting
se 1-phosphate and a nucleobase to form a deoxyribonucleoside
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Matches:
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Mismatches:
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                                                      Disclosure; Page 62-63; 73pp; English.
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                           deoxyribose
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The invention relates to a method for evolution of a protein (X) so as to modify its characteristics. Further disclosed are mutated proteins (X*) produced by the new method and with altered activity, relative to (X). Also disclosed is a nucleic acid (I) comprising a sequence for N-dideoxyribosyltransferase (DDTP), obtained from an N-geoxyribosyltransferase (DDTP), obtained from an N-geoxyribosyltransferase (DDTP), i.e. an enzyme able to transfer and dideoxyribosyltransferase (DDTP), i.e. an enzyme able to transfer dideoxyribosyltransferase (DDTP), i.e. an enzyme able to transfer addeoxyribosyltransferase (DDTP), i.e. an enzyme able to transfer and dideoxyribosyltransferase (DDTP), i.e. an enzyme able to transfer and dideoxyribosyltransferase and nucleosides that have antivity or can be used to treat infections, particularly ddc and ddI. The current sequence represents the N-deoxyribosyltransferase (DTP) amino acid sequence containing a G9S mutation. This protein
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Cytostatic; antimicrobial; N-dideoxyribosyltransferase; DDTP; N-deoxyribosyltransferase; DTP; antitumour; infection; ddC; ddI; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method for evolution of proteins to modify characteristics, useful particularly for evolving an N-deoxyribosyltransferase to produce an N-dideoxyribosyltransferase for preparation of antitumor nucleosides and nucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 TyrLysGluAlaMetGluAlaLeuLysGluAsnProThrileAspLeuGluAsnSerTyr
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                                                                                                                                                                 Location/Qualifiers
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(CNRS ) CNRS CENT NAT RECH
                                                                                            Lactobacillus leichmannii
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N-PSDB; ADR97104.
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136 CTGGACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCATGACAAG 195
                                                                                                                                          New N-deoxyribosyltransferase from Lactobacillus, useful for preparing deoxyribonucleotides, e.g. for use as antiviral agents, also related nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                 4 LysLysThrLeuTyrPheGlyAlaGlyTrpPheAsnGluLysGlnAsnLysAlaTyrLys
                                                                                                                            76 GAAGCCATGGAAGCCCTCAAGGAAAACCCAACGATTGACCTGGAAAACAGCTACGTTCCC
                                                                                                                                                                                                        196 GTTTGGGCTACGGCCACCTACAACAACGACTTGAACGGGATCAAGACCAACGACATCATG
                                                                                                                                                                                                                                                                      CTGGGTGTCTACATCCCTGACGAAGAGGTCGGCCTGGGCATGGAACTGGGTTACGCC
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                                                               AAAAAGACGATCTACTTCGGTGCCGGCTGGTTCACTGACCGCCAAAACAAAGCCTACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-deoxyribosyltransferase; ntd gene; enzyme; antitumour chemotherapy; deoxyribonucleotide synthesis; infection; insecticide; herbicide.
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                                  US-10-049-750-13 (1-483) x ABP98175 (1-158)
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(NARE-) INST NAT RECH AGRONOMIQUE.
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N-PSDB; ACC43585.
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                                                                                                                            The present sequence represents a N-deoxyribosyltransferase protein from Lactobacillus. The enzyme is encoded by the ntd gene. The N-deoxyribosyltransferase protein is useful to raise specific antibodies, and for in vitro or in vivo enzymatic synthesis of deoxyribonucleotides, particularly those containing non-natural bases. These deoxyribonucleotides are useful for treating bacterial, viral (e.g. HIV), parasitic or fungal infections, for antitumour chemotherapy, and as insecticides or herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New N-deoxyribosyltransferase from Lactobacillus, useful for preparing deoxyribonucleotides, e.g. for use as antiviral agents, also related nucleic acid and antibodies.
TACGCCTTGAGCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACTACGGCAAG
                                               250 ATCATGCTGGGTGTCTACATCCCTGACGAAGAAGACGTCGGCCTGGGCATGGAACTGGGT
                                                                                                                                                                         CCGATCAACCTCATGAGCTGGGGCGTCAGCGACAACGTGATCAAGATGAGCCAGCTGAAG
                                                                 81 IleMetLeuGlyValTyrIleProAspGluGluAspValGlyLeuGlyMetGluLeuGly
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(NARE-) INST NAT RECH AGRONOMIQUE.
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N-PSDB; ACC43580, ACC43586.
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                                                                                                                                                                                                                                                 GACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCATGACAAGGTT 198
The present sequence represents a N-deoxyribosyltransferase protein from Lactobacillus. The enzyme is encoded by the ntd gene. The N-deoxyribosyltransferase protein is useful to raise specific antibodies, and for in vitro or in vivo enzymatic synthesis of deoxyribonucleotides, particularly those containing non-natural bases. These deoxyribonucleotides are useful for treating bacterial, viral (e.g. HIV), parasitic or fungal infections, for antitumour chemotherapy, and as insecticides or herbicides
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                                                                                                                                                                                                                                                                                                                             AAGACGATCTACTTCGGTGCCGGCTGGTTCACTGACCGCCAAAACAAAGCCTACAAGGAA
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Best Local Similarity:
                                                                              Sequence 159 AA
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decoxyribosyltransferase-II. The nucleoside decoxyribosyltransferase-II and the encoding gene are useful in an enzymatic preparation of a decoxynucleoside. The decoxynucleoside is useful as the raw material for various drugs. The present sequence represents the L. helveticus recombinant nucleoside decoxyribosyltransferase-II (ndtB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 LeuGluAsnGlnTyrLysGlylleArg1leAspGluHisProGluTyrLeuHisAsn1le
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGAGCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACTACGGCAAGCCGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence of N-deoxyribosyltransferase protein.
                                                                                                                                                                                                      present invention relates to a recombinant nucleoside
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114
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                             Enzymatic preparation of deoxynucleoside.
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                                                                                                                                                                  Claim 1; Page 10; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard, protein; 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-049-750-13 (1-483) x AAG66170
08-AUG-2000; 2000JP-00239443
                                                                                                                                                                                                                                                                                                                                                                                        5.38e-58
637.00
87.10%
73.55%
73.98%
                                  (YAMS ) YAMASA SHOYU
                                                                     WPI; 2002-299403/34
N-PSDB; ABL40579.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                    Sequence 158 AA;
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The present sequence represents a N-deoxyribosyltransferase protein from Lactobacillus. The enzyme is encoded by the ntd gene. The N-deoxyribosyltransferase protein is useful to raise specific antibodies, and for in vitro or in vivo enzymatic synthesis of deoxyribonucleotides, particularly those containing non-natural bases. These deoxyribonucleotides are useful for treating bacterial, viral (e.g. HIV), parasitic or fungal infections, for antitumour chemotherapy, and as insecticides or herbicides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New N-deoxyribosyltransferase from Lactobacillus, useful for preparing deoxyribonucleotides, e.g. for use as antiviral agents, also related nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 AlaSerAlaThrTyrHisAsnAspLeuValGlyIleLysSerSerAspIleMetLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 AACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCATGACAAGGTTTGG
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                                                                                                                                                                                                     N-deoxyribosyltransferase; ntd gene; enzyme; antitumour chemotherapy; deoxyribonucleotide synthesis; infection; insecticide; herbicide.
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                                                                                                                                                                         Amino acid sequence of N-deoxyribosyltransferase protein.
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                14-SEP-2001; 2001FR-00011911.
                                                                             ABP98178 standard; protein;
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96.43%
86.90%
47.04%
                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                    Lactobacillus crispatus.
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NAT RECH
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(NARE-) INST
                                                                                                                                          11-AUG-2003
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                                                                                                            ABP98178;
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                                                                                                                                                                                                                                                                                                                                   preparing
related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTACATCCCTGACGAAGAAGACGTCGGCCTGGGCATGGAACTGGGTTACGCCTTGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 AACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCATGACAAGGTTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ValTyrLeuProGluGluGluAspValGlyMetGlyMetGluLeuGlyTyrAlaLeuSer
 N-deoxyribosyltransferase; ntd gene; enzyme; antitumour chemotherapy;
deoxyribonucleotide synthesis; infection; insecticide; herbicide.
                                                                                                                                                                                                                                                                                                                                New N-deoxyribosyltransferase from Lactobacillus, useful for deoxyribonucleotides, e.g. for use as antiviral agents, also nucleic acid and antibodies.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                      (INSP ) INST PASTEUR.
(NARE-) INST NAT RECH AGRONOMIQUE
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629.00
96.99%
84.21%
73.05%
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                                              Lactobacillus amylovorus
                                                                                                                                                                                                                                                                                    WPI; 2003-313351/30.
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Query Match:
DB:
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                                                                                                            27-MAR-2003
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The present sequence represents a N-deoxyribosyltransferase protein from Lactobacillus. The enzyme is encoded by the ptd gene. The N-deoxyribosyltransferase protein is useful to raise specific antibodies, and for in vitro or in vivo enzymatic synthesis of deoxyribonucleotides, particularly those containing non-natural bases. These deoxyribonucleotides are useful for treating bacterial, viral (e.g. HIV), parasitic or fungal infections, for antitumour chemotherapy, and as insecticides or herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 AsnieuMetLeuAlaArgGlyValThrTrp---LeuGluProAsn-----AspPhe 146
                                                                                                                                                                                                                                                                   LeuHisiysProllevalLeuLeuProPheThrLysLysAspLysSerAlaTyrGluAla 129
                                                                                                                            GCTACGGCCACCTACAACGACTTGAACGGGATCAAGACCAACGACATCATGCTGGGT 261
                                                                                                                                                                                                                                 262 GTCTACATCCCTGACGAAGAAGACGTCGGCCTGGGCATGGAACTGGGTTACGCCTTGAGC 321
                                                                                                                                                                                                                                                                                                                                            322 CAAGGCAAG---TACGTCCTTTTGGTCATCCCGGACGAAGACTACGGCAAG---CCGATC 375
                                                                                                                                                             CAGTACAAGGGTATCCGGGTTGATGAACACCCCGGAATACCTGCATGACAAGGTT---TGG
                                                                50 GiniyrLysAspAlaArgValAspSerAspProAlaGlyValPheGlySerLeuGluTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- AGCTGGGGCGTCAGCGACACGTGATCAAGATG
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(NARE-) INST NAT RECH AGRONOMIQUE.
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N-PSDB; ACC43581.
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381
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                         322 CAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACTACGGCAAGCCGATCAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-deoxyribosyltransferase; ntd gene; enzyme; antitumour chemotherapy; deoxyribonucleotide synthesis; infection; insecticide; herbicide.
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NAT RECH AGRONOMIQUE.
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209.00
51.66%
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                                                                                                      70 TACAAGGAAGCCATGGAAGCCCTCAAGGAAAACCCAACGATTGACCTGGAAAACAGCTAC 129
                                                                                                                                                                                                      GP900; Iowa isolate; glycoprotein; antibody; cryptosporidiosis; competitive inhibition; attachment; invasion; ligand binding; sporozoite; merozoite; diarrhoea; protozoacide; domain 2; mucin-like.
                                                                                                                                                 61
                                                                                  10 ATGCCAAAAAAGACGATCTACTTCGGTGCCGGCTGGTTCACTGACCGCCAAAACAAAGCC 69
                                                                                                              GACGAAGACTACGGCAAGCCGATCAACCTCATG---AGCTGGGGCGTCAGC-----
                                                                                                                                  130 GTTCCCCTGGACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATAC----
                                                                                                                                                                184 CTGCATGACAAGGTTTGGGCTACGGCCACCTACAACGACGACTTGAACGGGATCAAGACC
                                                                                                                                                                                             244 AACGACATCATGCTGGGTGTCTACATCCTGACGAGGAGGACGTCGGCCTGGGCATGGAA
                                                                                                                                                                                                                           CTGGGTTACGCCTTGAGCCAAGCAAGTACGTCCTTTTGGTC-------ATCCCG
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       167
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36
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       Length:
Matches:
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                                                          US-10-049-750-13 (1-483) x ABP98176 (1-167)
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93US-00071880.
95US-00415751.
96US-00700651.
96US-0026062P.
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                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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01-JUN-1993;
03-APR-1995;
14-AUG-1996;
13-SEP-1996;
Alignment Scores:
Pred. No.:
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PA (REGC ) UNIV CALIFORNIA.

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Petersen C;
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New GP900 protein fragments and fusion proteins of Cryptosporidium
Py parvain, useful for detecting the presence of the parasite, and diagnosing
or treating Cryptosporidium infections by competitive inhibition of the
Py parvain, useful for detecting the presence of the parasite, and diagnosing
or treating Cryptosporidium infections by competitive inhibition of the
Py function of GP900.

XX

Claim 3; Col 71-72; S9pp; English.

XX

Cryptosporidium parvum. DNA encoding it, GP900 fragments, and fusion
CY
Cryptosporidium parvum. DNA encoding it, GP900 fragments, and fusion
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CYPTOSPORIATION of GP900 of Tragments are able to administration of anthiody of cryptosporidiosis treatment
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Sequence 216 AA;

---TGGAAGCCCTCAAGGAAAACCCAACGATTGACCTGGAAAACAGCTACGTTCCCCTGG 139 200 GGGCTACGGCCACCTACAACAACGACTTGAACGGGATCAAGACCAACGACATCATGCTGG 259 131 GIGICIACAICCCIGACGAGGAGGACGICGGCCIGGGCAIGGAACIGGGTIACGCCTIGA 319 GCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACTACGGCAAGCCGATCAACC 379 Thribithrihrihrihrihrihrihrihrihrihrihrihrihsiysiyseroihr 71 140 ACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCATGACAAGGTTT 216 26 . 67 . 3 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-10-049-750-13 (1-483) x AAB11729 (1-216) 8.82e-06 142.00 46.10% 29.22% 16.49% Percent Similarity: Best Local Similarity: 56 22 83 260 320 Query Match: DB:

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New GP900 protein fragments and fusion proteins of Cryptosporidium parvum, useful for detecting the presence of the parasite, and diagnosing or treating Cryptosporidium infections by competitive inhibition of the function of GP900.
140 ACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCATGACAAGGTTT 199
                                                                 260 GTGTCTACATCCCTGACGAAGAAGACGTCGGCCTGGGCATGGAACTGGGTTACGCCTTGA 319
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------Thrithr 177
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                                                                                                                    200 GGGCTACGGCCACCTACAACAACGACTTGAACGGGATCAAGACCAACGACATCATGCTGG
                                                                                                                                                         GCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACTACGGCAAGCCGATCAACC
                                                                                                                                                                                                              TCATGAGCTGGGGCGTCAACGTGATCAAGATGAGCCAGCTGAAGGACTTCAACT
                                                                                                                                                                                                                                                                 TCAACAAGCCGCGTTCGACTTCTACGAAGGTGCCGTATACT 481
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ThrThrThrThrAlaThrThrThrThrLysLysProThrThr 191
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ThrThrThrThrThrThrThrThrThr-
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95US-00415751.
96US-00700651.
96US-0026062P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method of detecting Cryptosporidium ibiological and environmental samples, and of diagnosing cryptosporidiosis. This involves obtaining a sample and contacting it with Cryptosporidium GP900, P68 or cryptospain antigen, antibody, DNA or RNA, or its variant, mutant or fragment. The method is also useful for detecting and identifying individual Cryptosporidium isolates based on the genetic characteristics, and for diagnosis of prior or concurrent Cryptosporidium infection. The present sequence is a C. parvum protein sequence used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting Cryptosporidium in biological and environmental samples and diagnosis of cryptosporidiosis involves, contacting the sample with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNA.
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                                                                                                                                                                                                                                                       Cryptosporidium detection; GP900; P68; cryptopain; cryptosporidiosis.
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                                                                     TCAACAAGCCGCGCTTCGACTTCTACGAAGGTGCCGTATACT
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Matches:
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                                                                                                                                                    ABJ04047 standard; protein; 216 AA
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                                                                                                                                                                                                                                                                                    Cryptosporidium parvum
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Best Local Similarity:
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administration of GP900 or fragments thereof to a host to elicit anti-
GP900 antibody production, and to a method of cryptosporidiosis treatment
or prophylaxis comprising administration of enti-GP900 antibodies to an
individual. Cryptosporidium parvum GP900 and GP900 antibodies to an
individual. Cryptosporidium parvum GP900 and GP900 antibodies. The
competitively inhibit sporozoite or merozoite attachment or invasion, and
are also useful for the generation of anti-GP900 antibodies. The
antibodies also inhibit the binding of GP900 ligands to GP900. GP900
contenins, fragments and antibodies may therefore be used to treat or
prevent cryptosporidiosis. Infection with Cryptosporidium is a common
cause of diarrhoea in humans and causes life-threatening diarrhoea in
immunocompromised persons. Cryptosporidiosis can be contracted from
contaminated municipal water supplies (e.g., public swimming pools). It
is also a cause of disease in animals, resulting in financial losses in
agriculture. GP900 fragments, fusion proteins and antibodies may also be
used for the diagnosis of Cryptosporidium parvum infections, and for the
contaminated parasite in the environment. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATGAGCTGGGGCGTCAGCGACACGTGATCAAGATGAGCCAGCTGAAGGACTTCAACT 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGCTACGGCCACCTACAACAACGACTTGAACGGGATCAAGACCAACGACATCATGCTGG
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The present invention relates to a method of detecting Cryptosporidium in biological and environmental samples, and of diagnosing cryptosporidiosis. This involves obtaining a sample and contacting it with Cryptosporidium GP900, PG8 or cryptosporian antigen, antibody, DNA or RNA, or its variant, mutant or fragment. The method is also useful for detecting and identifying individual Cryptosporidium isolates based on the genetic characteristics, and for diagnosis of prior or concurrent Cryptosporidium infection. The present sequence is a C. parvum protein sequence used in the exemplification of the invention
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            Cryptosporidium detection; GP900; P68; cryptopain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New GP900 protein fragments and fusion proteins of Cryptosporidium parvum, useful for detecting the presence of the parasite, and diagnosing or treating Cryptosporidium infections by competitive inhibition of the function of GP900.
                                                                                                                                                                                                                                                                                             GP900; NINC isolate; glycoprotein; antibody; cryptosporidiosis; competitive inhibition; attachment; invasion; ligand binding; sporozoite; merozoite; diarrhoea; protozoacide; domain 2; mucin-like; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunocompromised persons. Cryptosporidiosis can be contracted from contaminated municipal water supplies (e.g., public swimming pools). It is also a cause of disease in animals, resulting in financial losses in agriculture. GP900 fragments, fusion proteins and antibodies may also be used for the diagnosis of Cryptosporidium parvum infections, and for the detection of the parasite in the environment. The present sequence represents a variant of the mucin-like domain 2 (AAB11734) of the Cryptosporidium parvum NINC isolate GP900 protein (AAB11727)
 --ThrThrThr 485
                                                                                                                                                                                                                                                         C. parvum NINC isolate GP900 variant domain 2, SEQ ID NO:20.
                                     440 TCAACAAGCCGCGCTTCGACTTCTACGAAGGTGCCGTATACT 481
                                                            474 ThrThrThrThrThrThrThrThrThr
                                                                                                                                                 AAB11746 standard; protein; 249 AA
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96US-00700651.
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Alignment Scores:

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122 ACAGCTACGTTCCCCTGGACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAAT 181
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                                                                                                     TATACTAAATGCCAAAAAAGACGATCTACTTCGGTGCCGGCTGGTTCACTGACCGCCAAA
                                                                                                                   302 AACTGGGTTACGCCTTGAGCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACT
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Disclosure; Page 128-129; 157pp; English

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The present invention relates to a method of detecting Cryptosporidium in
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Search completed: December 23, 2005, 22:29:56 Job time : 96.6485 Becs

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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Total number

Searched:

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Sequence 8, Application US/08928361B
Sequence 8, Application US/08928361B
Patent NO. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25861, A
Sequence 17597, A
Sequence 19857, A
Sequence 25549, A
Sequence 8, Appli
Sequence 13, Appli
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                                                                                                 22507, A
428, App
13, Appl
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15, Appl
15, Appl
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Sequence 18, Appl
Sequence 18, Appl
Sequence 25861, A
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
US-09-588-995A-17

US-09-216-333B-341

US-09-216-333B-341

US-09-216-333B-341

US-09-252-91A-22507

US-09-252-91A-28158

US-09-252-91A-28158

US-09-252-91A-28158

US-09-252-91A-28158

US-09-252-91A-2816

US-09-252-91A-28161

US-09-253-91A-28161

US-09-288-915A-14
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REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY AGENT INFORMATION:
NAME: Verny, Hana
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       Command line parameters:
-MODEL=frame+ n2: model -DEV=xlp
-MODEL=frame+ n2: model -DEV=xlp
-MODEL=frame+ n2: model -DEV=xlp
-De-/cgn2_1/USFTO_spool_D/US10049750/runat_23122005_113553_6317/app_query.fasta_1.1742
-DB=/sgaued_Patentes_AA -OFMT=fasta -SUPFIX=n2p.rai_-MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STATR=1 -END=-1 -MATRIX=blosmac2 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pet -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL_-OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLENE0 -MAXLENE=200000000
-USRR=US10049750_GCGN_1 1_101_@runat_23122005_113553_6317 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBBLOCK=100 -LONGLOG
-DSW TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                       December 23, 2005, 22:17:41; Search time 19.609 Seconds (without alignments) 4072.865 Million cell updates/sec
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Sequence 5, Appli
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1: ./cgn2_6/prodate/1/laa/5_COMB.pep:*
1: ./cgn2_6/prodate/1/laa/6_COMB.pep:*
3: ./cgn2_6/prodate/1/laa/H_COMB.pep:*
4: ./cgn2_6/prodate/1/laa/H_COMB.pep:*
5: ./cgn2_6/prodate/1/laa/RE_COMB.pep:*
6: ./cgn2_6/prodate/1/laa/RE_COMB.pep:*
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Compugen Ltd.
                                                                                                                          protein search, using frame_plus_n2p model
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US-09-588-995A-8
US-09-988-995A-5
US-08-928-361B-5
US-08-951-15
US-08-95A-20
US-08-700-651-5
US-08-95A-20
US-08-95A-6
US-08-995A-6
US-08-995A-6
US-08-995A-6
US-08-995A-6
US-08-995A-6
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                             GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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, Ygapext
, Fgapext
, Delext
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Maximum DB seq length: 2000000000
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861
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Database :

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Result

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RESULT 3
US-08-928-361B-5
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US-09-588-995A-8
; Sequence 8, Application US/09588995A
; Patent No. 6514697
; GENERAL INFORMATION:
; APPLICANT: BETERSEN.
; APPLICANT: BETERSEN.
; APPLICANT: BARNES, DEBRA A.
; APPLICANT: BARNES, DEBRA A.
; APPLICANT: GUT, JIEL
; TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES AND
; TITLE OF INVENTION: INFECTIONS
; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 480.19-5
; CURRENT APPLICATION NUMBER: US/09/588,995A
; CURRENT FILING DATE: 1997-03-27
; PRIOR PILING DATE: 1997-03-27
; PRIOR PILING DATE: 1997-09-12
; PRIOR FILING DATE: 1997-09-12
; PRIOR FILING DATE: 1997-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ThrThr 177
                                                                                                                                                                                                                                                                                                                                                                                                                                    200 GGGCTACGGCCACCTACAACGACTTGAACGGGATCAAGACCAACGACATCATGCTGG 259
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166 ThrThrThrThrThrThrThrThr--------
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45
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Mismatches:
Indels:
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                                                                                                                                                   Length:
Matches:
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           œ
                                                                                                                                                 1.97e-07
142.00
46.10%
29.22%
                                          LENGTH: 216 amino acids TYPE: amino acid
TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        16.49%
                                                                 STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                       Alignment Scores:
                                                                                                             US-08-928-361B-8
                                                                                                                                                                                                         Query Match:
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                                                                                                                                                                   Score:
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GENERAL INFORMATION:

APPLICANT: PETERS, CAROLYN

APPLICANT: PETERS, CAROLYN

TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS

TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS

TITLE OF INVENTION: SPECIES INFECTION/DIAGNOSIS OF CRYPTOSPORIDIUM

TITLE OF INVENTION: SPECIES INFECTIONS

NUMBER OF SEQUENCES: 30

CORRESPONDENCES: 30

CORRESPONDENCES: BIKSA

ADDRESSEE: PETERS, VENYY, JONES & BIKSA

STREET: 385 Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 GTGTCTACATCCCTGACGAAGAAGACGTCGGCCTGGGCATGGAACTGGGTTACGCCTTGA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 TCATGAGCTGGGGCGTCAGCGACAACGTGATCAAGATGAGCCAGCTGAAGGACTTCAACT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---ThrThrThr 177
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                            US-10-049-750-13 (1-483) x US-09-588-995A-8 (1-216)
                                                                                                                                                                                                                                  Length:
Matches:
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                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                        Gaps:
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SEQ ID NO 8
LENGTH: 216
TYPE: PRT
TYPE: PRT
CRANKEN: Cryptosporidium parvum
US-09-588-995A-8
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                   142.00
46.10%
29.22%
16.49%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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BARNES, DEBRA A.
NELSON, RICHARD C.
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                            LENGTH: 1837
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                                                                                                                                                                                                                                                                                         TYPE: PRT
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45
26
67
16
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-049-750-13 (1-483) x US-08-928-361B-5 (1-1837)
                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,361B
BILING DATE: 12-SEP-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEFPAN: 650-324-1677
TELEFPAN: 650-324-1677
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
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474 ThrThrThrThrThrThrThrThr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09588995A Patent No. 6514697 GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
                                                                                                                                                                                                                                                                                                                                                        4.79e-07
142.00
46.10$
29.22$
16.49$
                                                                                                                                                                                                                                              LENGTH: 1837 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                            linear
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                          TOPOLOGY:
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APPLICANT: MELSON, RICHARD C.
APPLICANT: MELSON, RICHARD C.
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT APPLICATION NUMBER: US/09/589,95A
PRIOR FILING DATE: 1997-03-27
PRIOR PILING DATE: 1997-09-12
PRIOR PILING DATE: 1997-09-12
PRIOR PILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 ---TGGAAGCCCTCAAGGAAAACCCAACGATTGACCTGGAAAACAGCTACGTTCCCCTGG 139
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Mismatches:
Indels:
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Matches:
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; Sequence 15, Application US/08700651B
; Patent No. 6015882
; RENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Cryptosporidium parvum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.79e-07
142.00
46.10%
29.22%
16.49%
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NUMBER OF SEQUENCES:
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Best Local Similarity:
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TELEFAX: 6
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                                                DNAS AND RNAS
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: NELSON, RICHARD, C.
APPLICANT: NELSON, RICHARD, C.
APPLICANT: NUMBER: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS;
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TILE OF INVENTION: INFECTIONS
TILE OF INVENTION: INFECTION OF 651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 15
SEQ ID NO 15
LENGTH: 249
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
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; Patent No. 6071518
; GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPE
; TITLE OF INVENTION: FOR TREATMENT AND TITLE OF INVENTION: SPECIES INFECTIC
                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Cryptosporidium parvum
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138.50
43.75%
27.50%
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                 FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                 Score:
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182 ACCTGCATGACAAGGTTTGGGCTACGGCCACCTACAACGACTTGAACGGGATCAAGA 241
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ZIP: 94304-1840
COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA STREET: 385 Sherman Avenue, Suite 6 CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, V CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
RETERENCE/DOCKET NUMBER: 480
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 20:
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138.50
43.75%
27.50%
16.09%
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DNAS AND RNAS

us-10-049-750-13.n2p.rai

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S, GLYCOPROTEINS, DNAS AND OF Cryptosporidium parvum
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422 AGCTGAAGGACTTCAACTTCAACAGCCGCGCTTCGACTTCTACGAAGGTGCCGTATACT
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44
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                                                                                                      Sequence 5. Application US/08700651B
Patent No. 6015882
GENERAL INFORMATION:
APPLICANT: EEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GL;
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GL;
TITLE OF INVENTION: NOR PROPHILAXIS AND TREATMENT OF C;
TITLE OF INVENTION: INPECTIONS
FILE REFERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: 08/0700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER PELICATION NUMBER: 08/415,751
MUMBER OF SEQ ID NOS: 15
SEQ ID NO 5
SEQ ID NO 5
SEQ ID NO 5
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Matches:
Conservative:
Mismatches:
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ORGANISM: Cryptosporidium parvum
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                                                                                                                                                                                                                                                      SPECIES AND
                  AGCTGAAGGACTTCAACTTCAACAAGCCGCGCTTCGACTTCTACGAAGGTGCCGTATACT
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                                                                                                                                                                        APPLICANT: PETERSEN, CARCLIN
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, BERRA A.
APPLICANT: BARNES, BIRTHARD C.
APPLICANT: BARNES, BIRTHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION UNMERS: US/09/588,995A
CURRENT FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-04
PRIOR FILING DATE: 1996-08-04
PRIOR FILING DATE: 1996-08-14
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                                                                                                            Sequence 20, Application US/09588995A
Patent No. 6514697
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Best Local Similarity:
Query Match:
DB:
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422
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BEARNES, DEBRA A.
APPLICANT: BEARNES, DEBRA A.
APPLICANT: BELSON, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
CURRENT PAPLICATION NUMBER: 08/92/6.09-6-06
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR PILING DATE: 1997-09-12
PRIOR PILING DATE: 1996-08-14
PRIOR PILING DATE: 1996-08-14
PRIOR PILING DATE: 1996-08-14
PRIOR PILING DATE: 1996-08-14
PRIOR PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
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Mismatches:
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Patent No. 6514697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Cryptosporidium parvum
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Best Local Similarity:
Query Match:
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GENERAL INFORMATION:
APPLICAMY: PETERSEN, CAZOLYN
APPLICAMY: PETERSEN, CAZOLYN
TITLE OF INVENTION: PEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: PEPTIDES, PETERS, VARIANTS, ANALOGS AND FRAGMENTS;
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VENY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 ACCTGCATGACAAGGTTTGGGCTACGCCCACCTACAACAACGACTTGAACGGGATCAAGA 241
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY AGENT INFORMATION:
NAME: Verny, Hana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480.76-1 (HV)
                                                                                                                                                                                                                                                                                                                             ZIP: 94306-1840
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                               Sequence 6, Application US/08928361B Patent No. 6071518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480
TELECOMMUNICATION: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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138.50
43.12%
27.50%
16.09%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                COUNTRY:
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PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
                                                                                                                                                                               362 ACGGCAAGCCGATCAACCTCATGAGCTGGGGCGTCAGCGACAACGTGATCAAGATGAGCC 421
                                                                                                                                                    422 AGCTGAAGGACTTCAACTTCAACAAGCCGCGCGTTCGACTTCTACGAAGGTGCCGTATACT 481
--ThrThrThrThrThrThrThrThrThrThr 113
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FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
                                                                                                                                                                                                                                                                                               Sequence 17, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
TITLE OF INVENTION: PEPTIDES, POLYPE
TITLE OF INVENTION: THEIR FUNCTIONAL
TITLE OF INVENTION: SPECIES INFECTION
TITLE OF INVENTION: SPECIES INFECTION
TITLE OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: PETERS, VERNY, JONES & 385 Sherman Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatit
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Best Local Similarity:
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APPLICANT: PETERSEN, CAROLYN

APPLICANT: BETERSEN, CAROLYN

APPLICANT: BETERSEN, CAROLYN

APPLICANT: ARLSON, RICHARD, C.

APPLICANT: MISSON, RICHARD, C.

APPLICANT: GUT, JIRI

TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS;

TITLE OF INVENTION: INFECTIONS

FILE REFERENCE: 480.19-4(HV)

CURRENT APPLICATION NUMBER: US/08/700,651B

CURRENT FILING DATE: 1995-08-14

EARLIER APPLICATION NUMBER: US/08/15,751

EARLIER FILING DATE: 1995-04-03

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 12

LENGTH: 175

MANDER OF DELICEMENT OF THE OFFICE OFFICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNAS AND RNAS
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                                                                                                                                                                                                                                                                               ACCTGCATGACAAGGTTTGGGCTACGCCCACCTACAACAACGACTTGAACGGGATCAAGA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAAAGCCTACAAGGAAGCCATGGAAGCCCTCAAGGAAAACCCAACGATTGACCTGGAAA 121
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                                                                                302 AACTGGGTTACGCCTTGAGCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACT
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Cryptosporidium parvum
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134.50
43.12%
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Best Local Similarity:
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US-08-700-651-12
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86, Appl 62735, A 244659, 3, Appli 132077,

72004, A 57433, A

109125,

4395, Ap 59594, A

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TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND TITLE OF INVENTION: USES THEREOF FILE REPERBNCE: TX-1-C2 CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT PILING DATE: 1999-12-18
EARLIER APPLICATION NUMBER: 08/994,825
EARLIER PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                             Sequence 1883, Ap
Sequence 12, Appl
Sequence 1883, Ap
Sequence 109124,
Sequence 59602, A Sequence 68177, A Sequence 51579, A Sequence 46621, A Sequence 40384, A Sequence 62755, A Sequence 62755, A Sequence 62755, A
                                                                                                                                                                                                                   Sequence 53161, A Sequence 2004, App Sequence 3, Appli Sequence 39407, A Sequence 196, App Sequence 196, App Sequence 5566, App
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                                                                                                                                                                               Sequence 5
Sequence 4
Sequence 5
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Sequence
Sequence
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           US-10-425-114-68177

US-10-425-114-61578

US-10-425-114-46621

US-10-425-114-46621

US-10-425-114-40384

US-10-626-813-86

US-10-626-813-86

US-10-425-115-244659

US-10-425-115-244659

US-10-425-115-244659

US-10-425-115-244659

US-10-425-114-59594

US-10-425-114-59595

US-10-425-114-65068

US-10-437-963-109124

US-10-437-963-114-65068
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Matches:
Conservative:
Mismatches:
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Patent No. US20010014447A1
GENERAL INFORMATION:
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Best Local Similarity:
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Sequence 341, App
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Sequence 342, App
Sequence 36210, A
Sequence 22016, A
Sequence 59190, A
Sequence 59190, A
Sequence 53603, A
Sequence 53603, A
                                                                                           ; Search time 85.1442 Seconds (without alignments) 4740.464 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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                GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                     protein search, using frame_plus_n2p model
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US-09-216-393-344
US-10-321-856-344
US-10-321-856-344
US-11-09-143-36210
US-09-801-368-428
US-10-45-114-59190
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US-10-425-114-58693
US-10-425-114-56484
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                                                                                                December 23, 2005, 22:42:49
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Scoring table:

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Sequence 341, Application US/10321856

Publication No. US20030194393A1

GENERAL INFORMATION:
GENERAL INFORMATION:
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TYTLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THERE
TILE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THERE
FILE REFERENCE: TX-1-C2-1
CURRENT FILING DATE: 109/216, 393
PRIOR APPLICATION NUMBER: 09/216, 393
PRIOR PILING DATE: 1998-12-19
PRIOR APPLICATION NUMBER: 09/994, 825
PRIOR PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE PATENTIN Version 3.1
SEQ ID NO 341
LENGTH: 288
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  ----ThrThrProThrThrThrThrThrThrThrThrThrThrProThr 215
                                              248 ACATCATGCTGGGTGTCTACATCCCTGACGAAGAAGACGTCGGCCTGGGCATGGAACTGG 307
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Sequence 344, Application US/09216393
Patent No. US20010014447A1
GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: TX-1-C2
CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT FILING DATE: 1998-12-18
EARLIER PILING DATE: 1998-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 344
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ORGANISM: Toxoplasma gondii
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513 ThrThrThrLygArgProThrThrValThrGlubysThrSerSerAlaThrGlubysPro
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                                                                                      TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DECECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DECECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DECECTION ENERS.
FILE REPERENCE: CLOO0728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-03-23
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Mismatches:
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Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36210
LENGTH: 1795
              sequence 36210, Application US/11097143; Publication No. US20080208858A1; Publication No. US20080208858A1; APPLICANT: Venter, J. Craig
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14.63%
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Query Match:
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US-11-097-143-36210
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                                                                                                                                                                                  Sequence 344, Application US/10321856
Publication No. US20030194393A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER TILE REFERENCE: TX-1-C2-1
GURRENT FILING DATE: 109/216,393
PRIOR APPLICATION NUMBER: 09/216,393
PRIOR APPLICATION NUMBER: 09/94,825
PRIOR APPLICATION NUMBER: 09/94,825
PRIOR RILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: Patentin version 3.1
SEQ ID NO 344
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                       139 ArgSerLysArgGlyLysLysThrThrThrThrSerSerSerThrSerThrSerThr 158
AGCCGATCAACCTCATGAGCTGGGGCGTCAGCGACAACGTGATCAAGATGAGCCAGCTGA 427
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216 ThrThrThrThrThrThrProThrThr-----
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                                                                                                262 ThrThrSerThrThrThrThrThrThrThrThrThrThrThrThrProSerThr 279
                                                                           428 AGGACTICAACITCAACAGCCGCGCTICGACTICTACGAAGGIGCCGTAIACT
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ORGANISM: Toxoplasma gondii
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Best Local Similarity:
Query Match:
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US-10-321-856-344
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Blater, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Glaman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REPERENCE: 38-10(52052)8
CURRENT PAPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 6/360,039
PRIOR FILING DATE: 2002-02-21
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                 299 TGGAACTGGGGTTACGCCTTGAGCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAG 358
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-----SerThrSerThrThrSerProThrSerSerSerAlaPro
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Publication No. US20030233675A1
GENERAL INFORMATION:
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SEQ ID NO 22016
LENGTH: 605
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APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
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|ThrThrThrSerSerAlaProlleSerThrSerThrThrSerSerThrSerThr---- 261
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-- AlaSerThrThrThr 629
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                                 ---TCAACTTCAACA
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 613 HisArgProArgThrThrSerGlnLysThrThr
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Matches:
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CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
LENGTH: 605
                               107 TGATCAAGATGAGCCAGCTGAAGGACT----
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Royer, John
Salama, Sofie
Sherman, Amir
Silva, Jeff
                                                                                                    AGCCGCGCTTCGACTTCTACGAAG 469
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SerLysLeuSerThrThrThrGln 657
                                                                                                                                                                                                   ; Sequence 428, Application US/09801368; Patent No. US20020128250A1; GENERAL INFORMATION:
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Milne, Todd
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Best Local Similarity:
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US-09-801-368-428
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Qy         296 GCATGG	Publication No US2004006626A1   GENERAL INFORMATION:   APPLICANT: WELTNAUDR:   APPLICANT: WILLENWEG, GARRIELE   APPLICANT: TREFEZER, AREL   APPLICANT: TREFEZER, AREL   APPLICANT: BECHTHOLD. ANDREAS   TITLE OF INVENTION: AVILAMYCIN DERIVATIVES   TITLE OF INVENTION: AVILAMYCIN DERIVATIVES   FILE REPRENENCE: 1974-005   FILE REPRENENCE: 1974-005   FRICH APPLICATION NUMBER: PCT/EP01/09815   PRIOR APPLICATION NUMBER: DE 101 09 166.4   PRIOR APPLICATION NUMBER: DE 101 09 166.4   PRIOR APPLICATION NUMBER: DE 101 09 166.4   PRIOR PILING DATE: 2001-08-24   PRIOR PILING DATE: 2001-08-25   SOFTWARE: PALENTIN Ver: 3.2   SEQ ID NOS: 120   SOFTWARE: PALENTIN Ver: 3.2   TYPE: PRI	ORGANISM: Streptomyces viridochromogenes  i FRATURE: CTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.  OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.  US-10-084-846A-5  Alignment Scores: Pred, No.: Score: Conservative: 16 Best Local Similarity: 28.11	Gaps:  (0-13 (1-483) x US-10-084-846A-5 (1-19723)  1 TGCCAAAAAAGACGATCTACTTCGGTGCCGCCTGGTTCA	Qy         71 ACAAGGAAG           Db         9212 ThrargSerGlySerArgCysCysGlyProThrProSerArgSerProSerArgGlyArg           Qy         80           Bb         9232 SerThrThrSerSerThrTrpArgArgProProProProTrpThr1leTrpArgCysArg           Qy         86
Db 262SerThrSerThrThrSerProThrSerSerSerAlaPro 274  Oy 359 ACTACGGCARCAACCTCATGAGCTCAGGGACAACGTGATCAAGATGA 418	APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua APPLICANT: Shou, Yihua APPLICANT: Screen, Steven E APPLICANT: Screen, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Cao, Yongwei TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: NUMBER: US/10/425,114 FILE REPERRACE: 38-21(53313) B CURRENT FILING DATE: 2003-04-28 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 59190 LENGTH: 292 ITYPE: PRT TYPE: PRT ORGANISM: Zea mays FRATURE: CORGANISM: Can mays FRATURE: ORGANISM: Clone ID: 700377772_FLI.pep	Alignment Scores:		Qy         113 ACCTGGAAAACAGCTACCCTGGACAACCAGTACAAGGGTATCCGGGTTG 166           bb         :::              c1                       i::                          f1                       f2         ATGAACACCCGGAATACCTGCATGACAACATGGGCTA

	203 GlyGlnArgGlnArgProGlnLeuGlnGlnProValArgArgHisGlyGly 270 CCCTGACGAAGACGTCGGCCTGGCATGGAACTGGGTTACGCCTTGAGCCAAGGCAA [	RESULT 11 US-10-425-114-56484  US-10-425-114-56484  Sequence 56484, Application US/10425114  Publication No. US20040034888A1  GENERAL INFORMATION:  APPLICANT: Liu, Jingdong  APPLICANT: Liu, Yihua  APPLICANT: Screen, Steven E  APPLICANT: Screen, Steven E  APPLICANT: Cao, Yongwei  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  TITLE OF INVENTION: Nucleic Acid Molecules Acid Molecules  NUMBER OF SEQ ID NOS: 73128  NUMBER OF SEQ ID NOS: 73128  SEQ ID NO 56484  LENGTH: 347	ORGANISM: Zea mays PEATURE: -10-425-114-56484 -10-425-114-56484 ignment Scores: 0.00352 ed. No.: 119.00 reent Similarity: 42.47* eft Local Similarity: 13.82*	DB: 9  US-10-049-750-13 (1-483) x US-10-425-114-56484 (1-347)  Qy 75 GGAAGCCATGGAAGCCTCAAGGAAAACCCAACGATTGACCTGGAAAACAG 125	Qy         126
Qy         143 ACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCATGACA 193           Db         9292 ArgSerProArgalaThrGlyAlaThrSerThrArgSerAlaArgValArgCysThrThr 9311           Qy         194 AGGTTTGGGCTACCGCCACCT	215ACAACAACGACTTGAACGGATCAAGACCACGACTTGATGCTGG 215ACAACAACGACTTGAACGGATCAAGACCAACGACTTGATGCTGG 332 AlaLeuProAlaCysSerThrProThrAspArgGlyCysAlaAlaThrThrGlyGlyTrp 260 GTGTCTACATCCCTGACGAAG	Oy 380 TCATGAGCTGGGGCGCACAACG 406  [4]	CURRENT APPLICATION NUMBER: US/10/425,114  CURRENT FILING DATE: 2003-04-28  NUMBER OF SEQ ID NOS: 73128  SEQ ID NO 53603  LENGTH: 324  TYPE: PRT  ORGANISM: Zea mays  FRATURE:  CHAR INFORMATION: Clone ID: UC-ZMFLMO17202D01_FLI.pep	Alignment Scores: Alignment Scores: Cores: Core 119.00 Matches: Percent Similarity: Best Local Similarity: 32.88\$ Mismatches: 44 Query Match: DB:  A Gaps: Conservative: 14 Gaps: Conservative: 14 Gaps: A Gaps: Conservative: 14 Gaps: A A A A A A A A A A A A A A A A A A A	US-10-049-750-13 (1-483) x US-10-425-114-53603 (1-324)  Qy

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Sequence 68177, Application US/10425114
; Sequence 68177, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Careen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313) B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 68177
                                                                                                                                                  GlyLeuHisGlyGlyArgArgAlaLeu------ProGlyArgHisArgArgAla 208
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275 ValArgGluArgLeuAlaLeuGlyArgArgLeuArgGlyGlnArgArgGlnArgAlaGlu 294
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241 GlyGlnArgGlnArgProGlnLeuGlnGlnProValArgArgHisGlyGly-----
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US-10-425-114-68177
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Matches:
Conservative:
Mismatches:
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315 GlyAspLeuArgLeuArg 320
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Soreen, Steven E
APPLICANT: Rovalic, David K.
APPLICANT: Cao, Yongue, B
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongue, B
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Labaska, Jack E
APPLICANT: Labaska, Jack E
APPLICANT: Uson's Norieic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 18-21 (53313) B
CURRENT APPLICATION NUMBER: 1051-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 59602
LENGTH: 361
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                                                375 ---CAACCT-----CATGAGCTGGGGCGTCAGCGACAACGTGATCAAGATGAGCCAGCT 425
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                            ---CTACAACAACGACTTGAACGGGATCAAGACCAACGACATCATGCTGGGTGTCTACAT 269
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Publication No. US20040034888A1
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US-10-425-114-59602
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222 SerAlaGlyArgSerSerLeuGlyGluArgThrLysGluThrThrSerTrpTyrPro 240
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Job time : 99.1442 secs
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FEATURE:
                                                             US-10-425-114-53657
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APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Green, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NOWBER: US/10/425,114
SEQ ID NOS: 73128
SEQ ID NO 61578
                                 |||::: :::||||||| ::: |||
| ArgArgAlaThrArgProSerArgSerSerThrArgSerProAlaArgArgSerSerThr 146
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US-10-425-114-61578
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Matches:
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; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
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                                                                                                        316 GlyAspLeuArgLeuArg 321
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ORGANISM: Zea mays
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Sequence 53657, Application US/10425114

Publication No. U320040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 53867

LENGTH: 383
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US-10-425-114-53657
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Matches:
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Mismatches:
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Sequence 4, Appli
Sequence 36, App
Sequence 1065, App
Sequence 1065, Appl
Sequence 27, Appl
Sequence 17, Appl
Sequence 172, Appl
Sequence 202, Appl
Sequence 202, Appl
Sequence 28, Appl
Sequence 1034, Appl
Sequence 1034, Appl
Sequence 1034, Appl
Sequence 1034, Appl
Sequence 28, Appli
Sequence 28, Appli
Sequence 27, Appli
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Sequence 41, Appl
Sequence 16, Appl
Sequence 37, Appl
Sequence 39, Appl
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Sequence 12, Appl
Sequence 260, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1294, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PUJ480U2
CURRENT APPLICATION NUMBER: US/10/793,626
PRIOR PILING DATE: 1004-03-04
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SSCPTWARE: Patentin Ver. 2.1
SEQ ID NO 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 ACTAAATGCCAAAAAAGACGATCTACTTCGGTGCCGGCTGGTTCACTGACGCCCAAAACA
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Sequence 143
Sequence 31,
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US-11.094-586-7

US-11.137-465-36

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US-10-467-657-4172

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US-11-000-463-243

US-11-000-463-243

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US-11-000-463-243

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
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OTHER INFORMATION:
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US-10-793-626-1294
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Best Local Similarity:
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US-10-793-626-1294
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109, App
1068, Ap
219, App
252, App
100, App
4, Appli
914, Appl
211, Appl
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8: /cgn2 6/ptodata/2/pubpaa/USO3 NEW_PUB.pep:*
                 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                          frame_plus_n2p model
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US-10-873-228-109
US-11-108-172-1068
US-10-131-826A-219
US-10-485-217-252
US-11-102-240-100
US-11-108-172-1065
US-11-108-172-1065
US-10-851-231-44
US-10-858-730-21
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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499 ThrserAlaSerGluSerAlaSerThrSerAlaSerAlaSerAlaSerThrSerAlaSer 518
                                              59 AAAACAAAGCCTACAAGGAAGCCATGGAAGCCCTCAAGGAAAACCCAACGATTGACCTGG 118
                                                                                        519 AlaSerAlaSerThrSerAlaSerGlySerAlaSerThrSerThrSerAlaSerAlaSer 538
                                                                                                                                    119 AAAACAGCTACGTTCCCCTGGACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGG 178
                                                                                                                                                                                                                                                                                                                 239 AGACCAACGACA -- TCATGCTGGGTGTCTACATCCCTGACGAGAAGACGTCGGCCTGG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                    599 AlaSerAlaSerThrSerAlaSerAlaSerAlaSerThrSerAlaSerAlaSerThrSer 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            579 ThrSerAlaSerGluSerAlaSerThrSerAlaSerAlaSerAlaSerThrSerAlaSer
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559 GluSerAlaSerThrSerAlaSerGluSerAlaSerThrSerAlaSerAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 TCAGCGACAACGTGATCAAGATGAGCCAGCTGAAGGACTTCAACTTCAACAAGCCGCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFRENCE: 210121.471C15
CURRENT APPLICATION NUMBER: US/11/108,172
CURRENT APPLICATION NUMBER: US/11/108,172
PRIOR APPLICATION NUMBER: US/11/108,172
PRIOR APPLICATION NUMBER: US/11/108,172
PRIOR FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-04-10
PRIOR PILING DATE: 2000-08-28
PRIOR PRILING DATE: 2000-08-28
PRIOR PILING DATE: 2000-08-28
PRIOR PILING DATE: 2000-08-28
PRIOR PILING DATE: 2000-08-28
PRIOR PILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-19
PRIOR PILING DATE: 2000-06-19
PRIOR PILING DATE: 2000-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1068, Application US/11108172; Publication No. US2050260177A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meagher, Madeleine Joy
Stolk, John A.
Wang, Tongtong
Jiang, Yuqiu
Smith, Carole L.
King, Gordon E.
Wang, Aljun
Clapper, Jonathan D.
Skeiky, Yasir A. W.
Fanger, Gary R.
Vedvick Thomas S.
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                                                                                                                                                                                                                                                                                                                                                             126 ---ThrArgSerLysThrIleProThrSerVal---LysArgThrThrSerHisLysAla 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 GlnGlnSerThrLysSertHisThrThrSer---ValLysLysAsnThrThrGlnLeuSer 177
                                                                                                                                                         -----ACCCAACGATTGACC---TGGAAAACAGCTACGTTCCCCTGGACA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ACGGCAAGCCGATCAACCTCATGAGCTGGGGCGTCAGCGACAACGTGATCA 412
                                                                                                                                                                                                                                             182 ACCTGCATGACAAGGTTTGGGCTACGGCCACCTACAACAACGACTTGAACGGGATCAAGA 241
                                                                                                                                                                                                                                                                                                                                                                                                                            242 CCAACGACATCATGCTGGTGTCTACATCCCTGACGAAGAAGACGTCGGCCTGGGCATGG 301
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                                                                                          ||||||||:::|||
51 SerProThrGlnLysThrThrSerAsnPheLysArgSerValLysAspThrSerValLys 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTAPATGCCAAAAAAGACGATCTACTTCGGTGCCGGCTGGTTCACTGACC----
                                                                 65 AAGCCTACAAGGAAGCCA-----TGGAAGCCCTCAAGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             General 199, Application US/10873528
| Publication No. US20050276814A1
| GENERAL INFORMATION: APPLICANT: Microbial Technics Limited APPLICANT: Gilbert, Christophe FG APPLICANT: Gilbert, Christophe FG APPLICANT: Gilbert, Christophe FG APPLICANT: Gilbert, Christophe FG APPLICANT: Bansbro, Philip M FILLE REFERENCE: PWC/P21129W0
| CURRENT APPLICATION NUMBER: US/09/769,787 PRIOR APPLICATION NUMBER: US/09/769,787 PRIOR APPLICATION NUMBER: GB 9816337.1 PRIOR FILING DATE: 2001-01-26
| PRIOR FILING DATE: 1998-03-27 PRIOR FILING DATE: 1998-03-27 PRIOR FILING DATE: 1998-03-19
| NUMBER OF SEQ ID NOS: 388
| SOFTWARE: PARCHIN VET. 2.1
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43.37%
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Best Local Similarity:
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US-10-873-528-109
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------thrGlyThrGlyThrCysAlaAlaCysThrThr 813
                Smith, Victoria
Stewart, Timothy A.
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87.50
41.23$
30.70$
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US-10-131-826A-219
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 ACATCCCTGACGAAGAAGACGTCGGCCTGGGCATGGAACTGGGTTACGCCTTGAGCCAAG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 GCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACTACGGCAAGCCGATCAACCTCATGA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 GCTGGGGCGTCAGCGACAACGTGATCAAGATGAGCCAGCTGAAGGACTTCAACA 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 AAGCCCTCAAGGAAACCCAACGATTGACCTGGAAAACAGCTACGTTCCCCTGGACAACC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 CGGCCACCTACAACAACGACTTGAACGGGATCAAGACCAACGACATCATGCTGGGTGTCT 265
                                                                                                                                                                                                                                                                                                                                                                                                                       146 AGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCATGACAAGGTTTGGGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1691 ---ProProThrThrMetThrThrProSer---ProThrThr------
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: US 09/504,629
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-15
PRIOR PILING DATE: 2000-01-10
PRIOR PILING DATE: 1999-12-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1130
SEQ ID NO 1068
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Matches:
Conservative:
Mismatches:
Indels:
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; Sequence 219, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                         0.163
92.50
37.50%
28.29%
10.74%
                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-172-1068
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Abang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR PILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThralaalaThrThrGlyCysAlaCysAlaThrThrThrThrCysThrGlyThrGly 751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 AACTGGGTTACGCCTTGAGCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACT 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 219
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Mismatches:
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SerThrSerThrSerLeuSerAsnSerAlaSerAlaSerGluSerAspLeuSerSerThr 363
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Matches:
Conservative:
Mismatches:
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Sequence 252, Application US/10485517
Publication No. US20050256299A1
GENERAL INRORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Roster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629W0
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: PAECHILING PAECHILING DATE: 2002-01-09
INUMBER OF SEQ ID NOS: 424
SEQ ID NO 252
LENGTH: 761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 100, Application US/11102240; Publication No. US20050260647A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-252
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85.50
45.59%
28.68%
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TITLE OF INVENTION: ANTHRONIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESSIFILE OF INVENTION: BSOPHAGEAL TUMOR FILE OF INVENTION: BSOPHAGEAL TUMOR FILE REFERENCE: P3230RIC106C
CURRENT APPLICATION NUMBER: US/11/102,240
CURRENT FILING DATE: 2005-04-08
FRIOR PLING DATE: 2005-07-07
FRIOR APPLICATION NUMBER: 10/06867
FRIOR PLING DATE: 2000-08-24
FRIOR APPLICATION NUMBER: PCT/US00/23328
FRIOR APPLICATION NUMBER: PCT/US00/23328
FRIOR PLING DATE: 2000-08-24
FRIOR PLING DATE: 199-12-09
FRIOR FILING DATE: 199-12-09
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FRIOR FILING DATE: PSD-12-09
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|260 SerSerThrThrSerSerGlyAlaSerThrAlaThrAsnSerAspSerSerThrValSer 279
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---GluSerSerThrThrSer 294
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Publication No. US20050271625A1
GENERAL INFORMATION:
APPLICANT: Nash, Kevin R.
APPLICANT: Burger, Corinna
TITLE OF INVENTION: TAAV-NEPRILYSIN COMPOSITIONS AND METHODS OF USE
FILE REPERBUCE: 36689.8
CURRENT APPLICATION NUMBER: US/11/070,627
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79.50
44.22%
25.85%
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Wood, William I
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US-11-102-240-100
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US-11-070-627-4
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358 IleLeuThrLysTyrPheProArgAspPheGlnAsnLeuPheSerTrpArgPheIleMet 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 MetAsnLysValMetGluLeuGluLysGluIleAlaAsnAlaThrThrLysSerGluAsp 292
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Matches:
Conservative:
Mismatches:
Indels:
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; Sequence 1065, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Ku, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Stolk, John A.
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
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378 AspLeuValSerSerLeuSerArg 385
CURRENT FILING DATE: 2005-02-02
PRIOR APPLICATION UNMBRR: 60/549,399
PRIOR FILING DATE: 2004-03-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.3
SEQ ID NO 1750
                                                                                                                                           ; ORGANISM: Oryctolagus cuniculus US-11-070-627-4
                                                                                                                                                                                                                2.46
78.00
36.70%
23.40%
9.06%
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Best Local Similarity:
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NUMBER OF SEQ ID NOS: 1130
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1065
LENGTH: 957
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Ring, Adjun
APPLICANT: Skeiky, Yaair A. W.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Ranger, Gary R.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: Corter, Darrick
TITLE OF INVENTION: CORCONOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: CORCONOUNDS FOR IMMUNOTHERAPY
TITLE OF INVENTION: CORCONOUNDS FOR IMMUNOTHERAPY
TITLE OF INVENTION NUMBER: US 09/922,217
PRIOR APPLICATION NUMBER: US 09/922,217
PRIOR FILING DATE: 2001-08-03
PRIOR PLICATION NUMBER: US 09/649,811
PRIOR APPLICATION NUMBER: US 09/649,811
PRIOR APPLICATION NUMBER: US 09/675,251
PRIOR APPLICATION NUMBER: US 09/675,251
PRIOR APPLICATION NUMBER: US 09/675,251
PRIOR APPLICATION NUMBER: US 09/64629
PRIOR PLILING DATE: 2000-05-19
PRIOR PLILING DATE: 2000-05-19
PRIOR PLILING DATE: 2000-01-10
PRIOR PLILING DATE: 2000-01-10
PRIOR PLILING DATE: 2000-01-10
PRIOR PRIOR APPLICATION NUMBER: US 09/476,296
PRIOR PRIOR PLILING DATE: 2000-01-10
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Query Match:
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US-11-108-172-1065
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| AlaSerThrGlnThrGlyLeuProAlaThrLeuThrThrAlaAspLeuGlyGluGluSer 742
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---GlyThrThr 755
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                                                             377 ACCTCATGAGCTGGGGCGTCAGCGACAACGTGATCAAGATGAGCCAGCTGAAGGACTTCA 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 AAACAAAGCCTACAAGGAAGCCATGGAAGCCCTCAAGGAAAACCCAACGATTGACCTGGA 119
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                                                                                                                                                                                                                                                                         APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SEQ ID NO 914
SEQ OF NO 914
LENGTH: 1532
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Matches:
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||ThrThrPheProSerSerSerGlySerThr-
                                                                                                                              437 ACTICAACAAGCCGCGCTICGACTICI 463
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; Publication No. US20050255568A1
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42.11%
30.70%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-10-821-234-914
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US-10-858-730-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gargen, Nevin 1.
APPLICANT: O'Leary, Jessica
APPLICANT: O'Leary, Jessica
APPLICANT: O'Toole, George
APPLICANT: Walbridge, Michael J.
APPLICANT: Walbridge, Neter S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR AMINO ACID
CURRENT APPLICATION NUMBER: US 60/475,000
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 364
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 616
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US-10-641-678-62
; Sequence 62, Application US/10641678
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                                                                     Driggers, Edward M.
Madden, Kevin T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Thermobifida fusca
US-10-858-730-21
APPLICANT: Bailey, Richard B.
APPLICANT: Blomquist, Paul
APPLICANT: Doten, Reed
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167 sHisAspGlu 170
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 ------CCTACAACAACGACTTGA 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 AACACCCGGAATACCTGCATGACAAGGTTTGGGCTACGGCCA------
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                                    GENERAL INCOMMENTION;

GENERAL INCOMMENTATION;

APPLICANT: Goedegebuur, Frits

APPLICANT: Gualfetti, Peter

APPLICANT: Mitchinson, Colin

APPLICANT: Mitchinson, Colin

APPLICANT: Materinson, Mats

APPLICANT: Sandgren, Mats

APPLICANT: Stahlberg, Jerry

TITLE OF INVENTION: Cellulases

FILE REFERENCE: GC772-3

CURRENT APPLICATION NUMBER: US/10/641,678

CURRENT PILING DATE: 2003-09-15

PRIOR APPLICATION NUMBER: US 60/458,853

PRIOR FILING DATE: 2003-03-27

PRIOR FILING DATE: 2003-03-27
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Matches:
Conservative:
Mismatches:
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OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Penicillum janthinellum
US20050277172A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.4
75.00
40.68%
26.27%
8.71%
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Best Local Similarity:
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NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 48,
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Pred. No.:
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US-11-094-586-4
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DB:
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Sequence 4, Application US/11094586 Publication No. US20050273886A1

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190 rAspGlnIle-----TyrGlyAsnThrLeuSerIleSerGluIleLysTh 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTACAAGGAAGCCATGGAAGCCCTCAAGGAAAACCCAACGATTGACCTGGAAAACAGCTA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 MetSerAlaSerHis---AsnProGlyGlyProAspAsnAspTrpGlyIleLysPheAsn 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 ACTGGGTTACGCCTTGAGCCAAGGCAAGTACGTCCTTTTGGTCATC---CCGGACGAAGA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTACGGCAAGCCGATCAACCTCATGAGCTGGGGCGTCAGCGACAACGTGATCAAGATGAG 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 CGTTCCCCTGGACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGACAAGGTTTGGGCTACGGCCACCTACAACGACTTG-----AACGGGATCAAGAC
APPLICANT: Allen., Stephen M.
APPLICANT: Butler, Karlene H.
APPLICANT: Butler, Karlene H.
APPLICANT: Carlson, Thomas J.
APPLICANT: Stoop, Johan M.
TITLE OF INVENTION: Plastidic Phosphoglucomutase Genes
FILE REFERENCE: BB1451 USCIP
CURRENT APPLICATION NUMBER: US/11/094,586
CURRENT FILING DATE: 2005-03-30
FRIOR APPLICATION NUMBER: US 09/906,209
FRIOR APPLICATION NUMBER: US 09/906,209
FRIOR APPLICATION NUMBER: US 00/218,712
FRIOR FILING DATE: 2000-07-16
SROFWARR: Microsoft Office 97 & Patentin Version 3.3
SOFTWARR: Microsoft Office 97 & Patentin Version 3.3
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Conservative:
Mismatches:
Indels:
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Sequence 455, Application US/11000463

Publication No. US20050266423A1

GENERAL INPORMATION:

APPLICANT: Tang, Y Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Chen, Rui-hong
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74.50
43.26%
29.79%
8.65%
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Best Local Similarity:
Query Match:
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ORGANISM: Zea mays
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Pred. No.:
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| GlualaargGlnLeuarg-----GluargLeuGluGln-----Glu 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Zhiwel
APPLICANT: Wang, Zhiwel
APPLICANT: Wehrman, Tom
APPLICANT: Zhang, Jie
APPLICANT: Cao, Yi-Cheng
APPLICANT: Cao, Yi-Cheng
APPLICANT: Cao, Yi-Cheng
APPLICANT: OEGO, Yi-Cheng
FILE REFERENCE: PECPLON
CURRENT APPLICATION NUMBER: US/11/000,463
CURRENT FILING DATE: 2004-11-29
PRIOR PILING DATE: 2004-11-29
PRIOR PLING DATE: 2001-01-25
PRIOR PLING DATE: 2001-01-25
PRIOR PLING DATE: 2001-01-25
PRIOR PLING DATE: 2000-01-25
PRIOR PELICATION NUMBER: 09/491,404
PRIOR PLING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR PLING DATE: 2000-01-25
PRIOR PELING DATE: 2000-01-25
PRIOR PELING DATE: 2000-01-25
PRIOR PELING DATE: 2000-09-13
PRIOR PLING DATE: 2000-09-15
PRIOR PELING DATE: 2000-09-15
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NS-11-137-465-36

Sequence 36, Application US/11137465

Publication No. US2005025558A1

GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj

APPLICANT: Murdoch, Paul R.

APPLICANT: Smith, Randall, F.

APPLICANT: Smith, Randall, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.24
74.50
43.43
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Qian, Xiaohong
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ORGANISM: Homo sapiens
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Best Local Similarity:
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654 ------ProcysProaladlyThrPheGlnGluArgGluGlyGlnLeuSerCysAsp 670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 GGTTGTCCAGGGGAACGTAGC-----125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      432 GTCCTTCAGCTGGCTCATCTTGATCACGTTGTCGCTGACGCCCCAGCTCATGAGGTTGAT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 CTTGGCTCAAGGCGTAACCCAGTTCCATGCCCAGGCCGACGTCTTCTTCGTCAGGGATGT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------dalSerCysPro------GinGlyThr 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 AGACACCAGCATGATGTCGTTGGTCTTGATCCCGTTCAAGTCGTTGTTGTAGGTGGCCG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||||
708 ProCysProArgGlyThrTyrGlnProGluAlaGlyArgThrLeuCysPheProCysGly 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TGTTTTCCAGGTCAATCGTTG-----GGTTTTCCTTGAGGGCTTCCATGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 CGGCTTGCCGT-----AGTCTTCGTCCGGGATGACCAAAA---GGACGTACTTGC
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-049-750-13 (1-483) x US-11-137-465-36 (1-993)
APPLICANT: Kabnick, Karen
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50018
CURRENT APPLICATION NUMBER: US/11/137,465
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/10/239,663
PRIOR FILING DATE: 2002-09-24
PRIOR FILING DATE: 2001-03-22
PRIOR FILING DATE: 2001-03-22
PRIOR FILING DATE: 2001-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
SEQ ID NO 36
LENGTH: 993
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74.50
34.10%
26.59%
8.59%
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US-11-137-465-36
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GENERAL INFORMATION:

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132 Ile------ThrGluThrThrValLy8PheThrSerThrSerVallleThrSerVal 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 TITGGGCTACGGCCACCTACAACAACGACTTGAACGGGATCAAGACCAACGACATCATGC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 TGGGTGTCTACA-----TCCCTGACGAAGAAGACGTCGGCCTGGGCATGGAACTGGGTT 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 CGATCAACCTCATGAGCTGGGGCGTCAGCGACAACGTGATCAAGATGAGCCAGCTGAAGG 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::: ||| ||| ||| ||| ||| 92 GlnGlyThrPheSerAsnValSerThrAsnValSerTyrGlnGlyThrThrProSer 111
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| ThrLeuGlySerThrSerLeuHisProValSerGlnHisGlyAsnGluAlaThrThrAsn 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 GTGCCGGCTGGTTCACTGACCGCCAAAACAAAGCCTACAAGGAAGCCATGGAAGCCCTCA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
TILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SEQ ID NO 1065
LENGTH: 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      431 ACTICAACTICAACAAGCCGCGTTCGACTTCTACGAAGGTGCCGTATACT 481
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Matches:
Conservative:
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Indels:
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US-10-821-234-1065
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Best Local Similarity:
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-Q=/Cgn2_1/USPTO_spool_p/US10049750/runat_23122005_113553_6303/app_query.fasta_1.1742
-Q=/Cgn2_1/USPTO_spool_p/US10049750/runat_23122005_113553_6303/app_query.fasta_1.1742
-Q=/Cgn2_1/USPTO_spool_p/US10049750/runat_23122005_11-LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOODEZ=0.LOO
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                           frame_plus_n2p model
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Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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1: pir1:*
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nucleoside deoxyribosyltransferase (EC 2.4.2.6) II - Lactobacillus helveticus C; Species: Lactobacillus helveticus C; Species: Lactobacillus helveticus C; Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004 C; Accession: JC75.22; PC7103 R; Okuyama, K: Noguchi, T. Biotechnol. Biotechnol. Biother 64, 2243-2245, 2000 A; Title: Molecular cloning and expression of the nucleoside deoxyribosyltransferase-II g A; Reference number: JC7522; MUID:21012342; PMID:11129605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: PC7103
A;Molecule type: protein
A;Residues: 1-11;53-62 <OKZ>
A;Residues: 1-11;53-62 <OKZ>
A;Cross-references: UNIPARC:UP1000017A510; UNIPARC:UP1000017A511
C;Comment: This enzyme catalyzes transfer of glycosyl residues from a donor deoxynucleos
                                                                                                                                                                                                                                     antifreese glycope
chithase (EC 3.2.
glutenin high mole
glucan 1,4 alpha-g
salivary glue prot
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glutenin, high-mol
probable membrane
glutenin high mole
mucin SAC - human
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A;Residues: 1-158 < cKUJ.
A;Cross-references: UNIPROT:O9KWFO; UNIPARC:UPI000015C9E3; DDBJ:AB039914
A;Experimental gource: strain ATCC 8018
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C;Keywords: glycosyltransferase; pentosyltransferase
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T33922
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T34369
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A41258
T21460
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Wed Dec 28 10:16:52 2005

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                                                                                          CTGGGTGTCTACATCCCTGACGAAGAGACGTCGGCCTGGGCATGGAACTGGGTTACGCC 315
                                                                                                  AACCICATGAGCTGGGGCGTCAGCGACAACGTGATCAAGATGAGCCAGCTGAAGGACTTC 435
                                                                                                                                                               ---ATGAAC 172
                              CTGGACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCATGACAAG 195
                                                            GTTTGGGCTACGCCCACCTACAACAACGACTTGAACGGGATCAAGACCAACGACATCATG 255
                                                                                                                                       LeuserdindlyLysLeuPhePheTrpPheSerHisMetLysAspTyrGlyLysProlle 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TCAAGGAAAACCCAACGATTGACCTGGAAAACAGCTACGTTC 133
               43
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        ThrThrGluLysSerThrThrArgArgThrThrThrThrThrThrThrThrThrArg
GAAGCCATGGAAGCCCTCAAGGAAAACCCAACGATTGACCTGGAAAACAGCTACGTTCCC
                                      TTGAGCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACTACGGCAAGCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCCAAAAAAGACGATCTACTTCGGTGCCGGCTGGTTCACTGACCGCCAAAACA-----
                                                                                                                                                                                                                                                                                                                                                                           F;24-263/Product: Balivary glue protein sgs-3 #status predicted <MAT>
                                                                                                                                                                                    263
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27
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Matches:
Conservative:
Mismatches:
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150.50
44.20%
29.28%
17.48%
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Best Local Similarity:
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A;Cross-references: UNIPROT:096503; UNIPARC:UPI000007A269; EMBL:AF068065; NID:94063041; i
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R;Barnes, D.A.; Bonnin, A.; Huang, J.X.; Gousset, L.; Wu, J.; Gut, J.; Doyle, Mol. Biochem. Parasitol. 96, 93-110, 1998
A;Title: A novel multi-domain mucin-like glycoprotein of Cryptosporidium parrvu A;Reference number: Z20989; MUID:99066935; PMID:9851610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mucin-like glycoprotein 900 - Cryptosporidium parvum
C;Species: Cryptosporidium parvum
C;Spate: 22-0cr-1999 #sequence_revision 22-0cr-1999 #text_change 09-Jul-2004
||| ||||||:::|||
ProThrThrThrThrThrThrThrThrThrArgArgProThrThrArgSerThrThr
                                                                                 |||||||:::|||
116 ThrargHisThrThrThrThrThrThrArgArgProThrThrThrThrThrThr
                                                                                                                                                              ----ThrThrThrThr
                                                           173 ACCCGGAATACCTGCATGACAAGGTTTGGGCTACGGCCACCTACAACAACGACTTGAACG
                                                                                                                                        233 GGATCAAGACCAACGACATCATGCTGGGTGTCTACATCCCTGACGAAGAAGACGTCGGCC
                                                                                                                                                                                                                     293 TGGGCATGGAACTGGGTTACGCCTTGAGCCAAGGCAAGTACGTCCTTTTGGTCATCCCGG
                                                                                                                                                                                                                                            353 ACGAAGACTACGGCAAGCCGATCAACCTCATGAGCTGGGGCGTCAGCGACAACGTGATCA
                                                                                                                                                                                                                                                                                                                     413 AGATGAGCCAGCTGAAGGACTTCAACTTCAACAAGCCGCGCTTCGACTTCTACGAAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 ACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCATGACAAGGTTT
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Matches:
Conservative:
Mismatches:
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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435 ThrThrThrThrThrThrThrThrThr----
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142.00
46.10%
29.22%
16.49%
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Query Match:
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EMBL: Z49651; NID: 91015902; PI
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167 ThrSerThrThrProThrThrSerThrThrSerThrThrSer 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 ACCTGCATGACAAGGTTTGGGCTACGGCCACCTACAACAACGACTTGAACGGGATCAAGA 241
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ThrThrProThrThrSerThrThrSerThrThrProThrThrSerThrThrSerThrThr 206
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ProThrThrSerThrThrSerThrThrProThrThrSerThrThrSerThrThrProThr 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 ThrSerThrThrPro---ThrThrSerThrThrSerThrThrSerGlnThrSerThrLys 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                    probable membrane protein YJR1S1c - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein J2223; serine/threonine-rich protein YJR151c
CiSpecies: Saccharomyces cerevisiae
CiSpecies: 33-Aug-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
CiDate: 23-Aug-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
CiDate: T.
RiScarcez, T.
A;Reference number: S57169
A;Reference number: S57169
A;Reference number: S57169
A;Residues: 1-1161 <SCA>
A;Residues: 1-1161 <SCA>
A;Residues: 1-1161 <SCA>
A;Cross-references: UNIPROT:P47179; UNIPARC:UPI0000128E2A; EMBL:Z49651; NID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 SerThrThrSerThrThrProThrThrSerThrThrSerThrThrProThrThrSerThr
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T46740
microfilarial sheath protein SHP3 [imported] - Litomosoides sigmodontis
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: SGD:DAN4; MIPS:YJR151C
A;Cross-references: SGD:S0003912
A;Map position: 10R
C;Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                     hypothetical protein yejD [imported] - Lactococcus lactis subsp. lactis (strain IL1403) (Species: Lactococcus lactis subsp. lactis (C) Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004 (C) Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004 (C) Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004 (C) Malore Res. 11, 731-753, 2001 (C) Malore Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACATCATGCTGGGTGTCTACATCCCTGACGAAGAAGACGTC-----GGCCTGGGCATG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              409 ATCAAGATGAGCCAGCTGAAGGACTTCAACTTCAACAAGCCGCGCTTCGACTTCTACGAA 468
                                                                                                                                    --ThrThrThr 480
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                             380 TCATGAGCTGGGGCGTCAGCGACAACGTGATCAAGATGAGCCAGCTGAAGGACTTCAACT 439
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31 AsnAlaLeuSerLysAsnInsThrVal-----AlaAsnPhePheSerProMetArgCys 48
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  GCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACTACGGCAAGCCGATCAACC
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                                                                                                                                                                                                           440 TCAACAAGCCGCGCTTCGACTTCTACGAAGGTGCCGTATACT 481
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ThrThrThrThrThrThrThrThrThrThr
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26.71$
15.85$
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A;Molecule type: DNA
A;Residues: 1-605 <FAV>
A;Cross-references: UNIPROT:P38739; UNIPARC:UPI0000138FA0; EMBL:U11583; NID:92289854; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein YHL028w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S48940
R;Favello, T.
submitted to the EMBL Data Library, June 1994
A;Description: The sequence of S. cerevisiae cosmid 9196.
A;Reference number: S46794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: SGD:WSC4
A;Cross-references: SGD:S0001020; MIPS:YHL028w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                          A, Molecule type: mRNA
                                                                                                                                                                                                                                      C,Genetics:
A,Gene: GDB:MUC5AC
A,Cross-references:
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C;Species: Litomosoides sigmodontis
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46740
S;Hirzmann, J.
Submitted to the EMBL Data Library, October 1999
A;Reference number: Z23140
A;Reference number: Z23140
A;Residues: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-354 <HIR>
A;Conss-references: UNIPROT:Q25402; UNIPARC:UPI000008008D; EMBL:U54556; FIDN:AAB82017.2
C;Genetics: Shp3
A;Cons: Shp3

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mucin 5AC (clone JER47) - human (fragment)
C; Species: How sapiens man)
C; Species: Deceles: How sapiens man)
C; Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C; Accession: S53362; S71065
C; Accession: S53362; S71065
B; Student-Duperath, V; Audie, J.P.; Debailleul, V; Laine, A.; Buisine, M.P.; Galiegue-B; Studenen, J. 305, 211-219, 1995
A; Title: Characterization of the human mucin gene MUC5AC: a consensus cysteine-rich doma A; Reference number: S53361; MUID:95126907; PMID:7826332
A; Accession: S53362
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-477 cguy>
A; Residues: 1-477 cguy>
A; Residues: 1-477 cguy>
A; Residues: 1-477 cguy>
A; Experimental source: clone JER47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCATGACAAGGTTT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGCTACGGCCACCTACAACGACTTGAACGGGATCAAGACCAACGACATCATGCTGG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGTCTACATCCCTGACGAAGAAGACGTCGGCCTGGGCATGGAACTGGGTTACGCCTTGA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACTACGGCAAGCCGATCAACC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCATGAGCTGGGGCGTCAGCGACAACGTGATCAAGATGAGCCAGCTGAAGGACTTCAACT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ser-----SerThrThrLysProThrThrSerLysThrSerSer---ThrThrLysSer 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
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| ThrThrLysThrThrValLysThrSerThrThrThrLysThrThrThrSerSerThr
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53
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Mismatches:
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1133.50
49.33%
35.33%
15.51%
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A;Residues: 1-211,'S',213-224,'AR',227-259,'S',261-477 <POR>
A;Cross-references: UNIPARC:UP1000006D4B3; EMBL:Z34277; NID:9563374; PIDN:CAA84031.1; P11
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SerThrProSerGlyArgAlaThrSerProThrGlnSerThr---SerSerTrpGlnLys 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 SerArgThrThrLeuValThrThrSerThrThrSerThrPro---GlnThrSerThr 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 ThrSerAlaProThrThrSerThrThrSerAlaProThrThrSerThrThrSerAlaPro 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 CTGACGAAGAAGACGTCGGCCTGGGCATGGAACTGGGTTACGCCTTGAGCCAAGGCAAGT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGTCCTTTTGGTCATCCCGGACGAAGACTACGGCAAGCCGATCAACCTCATGAGCTGGG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 GCGTCAGCGACAACGTGATCAAGATGAGCCAGCTGAAGGACTTCAACTTCAACAAGCCGC 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 CCTACAACAACGACTTGAACGGGATCAAGACCAACGACATCATGCTGGGTGTCTACATCC
                                                                                                                                                                                                                                                                                                                                                               477
49
25
58
18
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Conservative:
Mismatches:
Indels:
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submitted to the EMBL Data Library, June 1994
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                                                                                                                                                                                                                                 OMIM:158373
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                                                                                                                                                                                                                                                      A, Map position: 11p15.5-11p15.5
C, Keywords: glycoprotein, tandem repeat
                                                                                                                                                   A; Experimental source: clone JER47
                                                                                                                                                                                                                                                                                                                                                            0.00141
128.00
49.33%
32.67%
14.87%
                                                                                                                                                                                                                              GDB:454136;
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                     A;Reference number: S71065
A;Accession: S71065
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A,NOTE: ORF71
C,Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1 glycoprotein homo
F,558-866/Domain: equine herpesvirus 1 glycoprotein homology <EHG>
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A;Cross-references: UNIPROT:039781; UNIPARC:UP10000ECBA1; EMBL:D88733; PIDN:BAA20037.1
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ThrAsnSerArgSerThrValSerAlaThrThrLysProThrProMetSerArgSerThr
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C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change
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R;Kirisawa, R.; Kobayashi, T.; Kawakami, Y.; Iwai, H.
J. Equine Sci. 7, 79-87, 1996
A;Title: Nucleotide sequences of open reading frames 1,
A;Reference number: 222973
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Mismatches:
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Conservative:
Mismatches:
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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H84824
En/Spm-like transposon protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H48424
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Niarman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A64420; MUD:20083487; PMID:10617197
A;Accession: H84824
A;Atatus: preliminary
A;Accession: H84824
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-510 <STO>
A;Cross-references: UNIPRRCT:004210; UNIPARC:UPI00000A9658; GB:AE002093; NID:g2088658; PI
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     A,Map position: 8L
C,Keywords: transmembrane protein
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A;Map position: 2
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C;Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1 glycoprotein homol
C;Keywords: glycoprotein; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-797/Product: glycoprotein X #status predicted <MAT>
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                                                                        224 ACTTGAACGGGATCAAGACCAACGACATCATGCTGGGTGTCTACATCCCTGACGAAGAAG
                                                                                             284 ACGTCGGCCTGGGCATGGAACTGGGTTACGCCTTGAGCCAAGGCAAGTACGTCTTTTTGG
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F:480-797/Domain: equine herpesvirus 1 glycoprotein homology <EHG>
F:766-790/Domain: transmembrane #status predicted <TMN>
F:500/Binding site: carbohydrate (Asn) (covalent) #status predicted
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97 ThrThrSerIleProThrSerThrSerThrGluThrThrThrThrThrThr
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A; Residues: 1-797 < TEL»
A; Cross-references: UNIPROT: P28968; UNIPARC: UPI00000138750; G
R; Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Virology 189, 304-316, 1992
A; Title: The DNA sequence of equine herpesvirus-1.
A; Title: The DNA sequence of equine herpesvirus-1.
A; Reference number: A41831; MUID: 9229566; PMID: 1318606
A; Contents: annotation; possible protein-coding frames
A; Note: neither amino acid nor nucleotide sequence is given
C; Genetics:
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C;Species: Xenopus laevis (African clawed frog)
C;Species: Ze-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: A45155
R;Hauser, F.; Hoffmann, W.
J;Biol. Chem. 267, 24620-24624, 1992
A;Title: P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 (FIM-C.: A;Reference number: A45155, MUID:93077556; PMID:1447205
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197 AlaThrThrThrAlaAlaThrThrAlaAlaThrThrThrThrAlaAlaThrThrThrAla 216
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                   CCATGGAAGCCCTCAAGGAAAACCCAACGATTGACCTGGAAAACAGCTACGTTCCCCTGG 139
                                                     ThrThrThrProThrThrThrAlaAlaProThrThrAlaAlaThrThrAlaVal 136
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                                                                                           ACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCATGACAAGGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-662 <HAU>
A;Cross-references: UNIPROT:Q05049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;162-202/Domain: trefoil homology
F;307-347/Domain: trefoil homology
F;354-394/Domain: trefoil homology
F;526-566/Domain: trefoil homology
F;573-613/Domain: trefoil homology
F;621-661/Domain: trefoil homology
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47.52%
31.21%
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Best Local Similarity:
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A;Molecule type: DNA
A;Residues: 1-232 <SW1>
A;Cross-references: UNIPROT:Q27423; UNIPARC:UPI000008094E; GB:X76203; NID:g433481; PIDN:
R;Lanio, W.; Swida, U.; Kress, H.
B;Colim: Biophys Acta 119, 576-580, 1994
A;Title: Molecular cloning of the Drosophila virilis larval glue protein gene Lgp-3 and A;Reference number: S50125; MUID:95002181; PMID:7918662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-232 <LA2>
A;Cross-references: UNIPARC:UPI000008094E; EMBL:229565; NID:g450901; PIDN:CAA82672.1;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: Glue protein genes in Drosophila virilis: their organization, developmental A,Reference number: A60095, MUID:90276249; PMID:2351069
                                                                                                                                         ACTACGGCAAGCCGATCAACCTCATGAGCTGGGGCGTCAGCGCAAACGTGATCAAGATGA 418
                                                                                                                                                                          ThrThrValProThrThrThrThrValProThrThrThrThrThrValProThrThr 485
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                                               TGGAACTGGGTTACGCCTTGAGCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAG 358
126 ValProThrThrThrThrValProThrThrThrThrValProThrThrThr 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            larval glue protein Lgp-1 precursor - fruit fly (Drosophila virilis)
C;Species: Drosophila virilis
C;Date: 03-Mar-1993 #sequence revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60095; S50126; $44060
R;Swida, U; Lucka, L; Kress, H.
Development 108, 269-280, 1990
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                                                                                            446 ThrValSerThrThrThrThrValProThrThrThrThrValSerThrThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: salivary glue protein
C;Reywords: glycoprotein; salivary gland; tandem repeat
C;Reywords: glycoprotein; salivary gland; tandem cspeat
F;1-13,Domain: slignal sequence #status predicted <SIG>
F;43-86,94-104,Region: 11-residue repeats (T-T-T-T-T-T-T-T-T-T)
F;105-160/Region: 8-residue repeats (T-T-T-T-T-T-P)
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A;Cross-references: FlyBase:FBgn0010305
A;Map position: X16A
A;Introns: 10/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F55B11.3 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C,Accession: T22696
R,Ainscough, R.
Submitted to the EMBL Data Library, December 1996
A,Reference number: Z18601
A,Reference number: Z18601
A,Reference number: Z18601
A,Residues: T22696
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-851 < WIL>
A,Residues: 1-851 < WIL>
A,Coss-references: UNIRROT:017893; UNIPARC:UPI00001641DA; EMBL:Z83318; PIDN:CAB
A,Experimental source: clone F55B11
C,Genetics:
A,Gene: CESP:F55B11.3
A,Map position: 4
A;Introns: 49/3; 123/3; 226/1; 282/3; 669/3; 743/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 ThralaThrSerThrProThrThrThrThrProThrSerThrThrThrThrThrAlaThr 171
                                                                                                                                                                                                                                                                                                                                               ------TGGGTGTCTACATCCCTGACGAAGAAGACGTCGGCCTGGGCATGGAAC 304
                                                                                                                                                                                                                                                                 172 ThrThrValProThrThrAlaSerThrThrThrAspThrThrAlaAlaThrThrThr 191
                                                                                                                                                                                                                                                                                                                   305 TGGGTTACGCCTTGAGCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACTACG 364
                                                                                                                                                                                                                                                                                                                                                                                                                GCAAGCCGATCAACCTCATGAGCTGGGGCGTCAGCGACCAACGTGATCAAGATGAGCCAGC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCATGACAAGG 196
                                                                      132 ThrThrThrAlaValThrThrAlaAlaSerThrSerAlaGluThrThrThrAlaThrAla 151
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Db 192 AlaAlaThrThrThrAlaAlaThrThrThrAlaAlaThrThrThrAlaAlaThrThrThr				
Db   94 ThrThrThrThrThrThrThrThrThrThrThrArgThr 107     09   182 ACCTGCATGACAAGGTTTGGGCTACGGCCTCAACAACAACGACTTGAACGGGATCAAGA 241	RESULT 15 745463 membrane glycoprotein [imported] - equine herpesvirus 1 C; Species: aquine herpesvirus 1 C; Species: equine herpesvirus 1 C; Species: aguine herpesvirus 1 C; Accession: T45463 M; Kilseawa, R.; Kobayashi, T.; Kawakami, Y.; Iwai, H. G; Accession: T45463 M; Aitle: Nuclectide sequences of open reading frames 1, 24 and 71 of an attenuated equin A; Reference number: 222973 M; Accession: T45463 M; Accession: T45463 M; Accession: Preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Molecule type: DNA A; Mesidues: 1-867 - KIRA A; Mesidues: 1-867 - KIRA A; Mesidues: 1-867 - KIRA A; Accession: Species: Solate 3F clone; strain BK343 C; Genetics: A; Mote: ORF71 C; Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1 glycoprotein home	Alignment Scores: Pred. No.: Pred. No.: Score: Score: Bercent Similarity: Best Local Similarity: 27.04	Oy 26 TCTACTTCGGTGCCGGCTGGTTCACTGACCGCCAAACAAA	Oy 137 TGGACAACCAGTACAAGGGTACACGGGTTGAACACCCGGAATACCTGCATGACAAGG 196  132 ThrThrThrAlaValThrThrAlaAlaSerThrSerAlaGluThrThrThrAlaThrAla 151  Oy 197 TTTGGGCTACGGCCACCTACAACAACGACTTGAACGGGATCAAGACCAACGACATCATGC 256  197 TTTGGGCTACGGCCACCTACAACAACGACTTGAACGGGATCAAGACCAACGACATCATGC 256  152 ThrAlaThrSerThrProThrThrThrProThrSerThrThrThrThrThrThrThrThrThrThrThrThrThr

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OM nucleic

Run on:

Scoring table:

Minimum DB Maximum DB

Searched:

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X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).

X Armstrong S.R., Cook W.J., Short S.A., Ealick S.E.;

Armstrong S.R., Cook W.J., Short S.A., Ealick S.E.;

"Crystal structures of nucleoside 2-deoxyribosyltransferase in native
"Crystal structures of nucleoside 2-deoxyribosyltransferase in native
"Tryptal structures of nucleoside reveal architecture of the active site.";

In and ligand-bound forms reveal architecture of the active site.";

Structure 4:97-107(1996).

In an all structure A:97-107(1996).

In con acceptor purine or pyrimidine base.

In carpatric Activity: 2-deoxy-D-ribosyl-base(1) + base(2) = 2-deoxy-

D-ribosyl-base(2) + base(1).

In dependence of the active site.";

PH dependence of the crystall properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE, PROTEIN SEQUENCE OF 1-25, FUNCTION, ACTIVE SITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Homohexamer. SIMILARITY: Belongs to the nucleoside deoxyribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND MUTAGENESIS OF GLU-97.

MEDLINE=95318137; PubMed=7797550; DOI=10.1074/jbc.270.26.15551;
Porter D.J.T., Merrill B.M., Short S.A.;
"Identification of the active site nucleophile in nucleoside 2-deoxyribosyltransferase as glutamic acid 98.";
J. Biol. Chem. 270:15551-15556(1995)
             04qqk4
025402
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08im89
04qqk1
04qqk1
06vax9
04bx73
06vax9
088814
06aw0
05cax1
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Lactobacillus.
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01-FEB-2005 (Rel. 46, Last annotation update)
Nucleoside deoxyribosyltransferase (EC 2.4.2.6) (N-
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                                          USCFZ6 CRYHO
Q25402 LITSI
Q8IMS9 DROME
Q4QGKI LBIMA
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Q86AK1_DICDI
Q76894_DROME
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PATHWAY: Nucleotide metabolism.
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Q6VAV6
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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Score

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                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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          CAUTION: Was originally (Ref.1) thought to originate from E.coli
                                                                                                                                                          Nucleophile.
E->A: Loss of transferase activity
3A3AEC3FD5B4743B CRC64;
                                                                                     PDB; 1F8X; X-ray; A/B=1-156.
PDB; 1F8Y; X-ray; A/B=1-156.
InterPro; 1FR007710; N deoxyrib trans.
Pfam; PF05014; Nuc_deoxyrib_tr; 1.
3D-structure; Direct protein sequencing; Nucleotide metabolism; Transferase.
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
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01-JUN-2002 (TEMBLEE). 21, La
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N-deoxyribosyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional cloning, heterologous expression, and purification of two different N-deoxyribosyltransferases from Lactobacillus helveticus."; J. Blol. Chem. 277:14400-14407(2002).
EMBL; AY064167; AAL73114-1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 AAAAAGACGATCTACTTCGGTGCCGGCTGGTTCACTGACCGCCAAAACAAAGCCTACAAG
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                  STRAIN=CNRZ32;
MEDLINE=21964041; PubMed=11836245; DOI=10.1074/jbc.M111995200;
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Bacteria; Firmicutes; Lactobacillales; Lactobacillus.
Lactobacillus.
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GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR007710; N deoxyrib_trans.
Pfam; PF05014; Nuc_deoxyrib_tr; 1.
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728.00
95.48%
82.58%
84.55%
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OSFMMB;
NUCLEOTIDE SEQUENCE
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[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
NCBI_TaxID=33959
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Percent Similarity:
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                                                    STRAIN=NCFM;
PubMed=15671160; DOI=10.1073/pnas.0409188102;
Altermann E., Russell W.M., Azcarate-Peril M.A., Barrangou R.,
Buck B.L., McAuliffe O., Souther N., Dobson A., Duong T., Callanan
Lick S., Hamrick A., Cano R., Klaenhammer T.R.;
"Complete genome sequence of the probiotic lactic acid bacterium
Lactobacillus acidophilus NCFM";
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Name-mid, OrderediocusNames=LJ0124;
Lactobacillus johnsonii.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
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EMBL; CP000033; AAV42046.1; -; Genomic_DNA.
GO; GO:0016740; Firtansferase activity; IEA.
Interpro; IPR007710; N decxyrib_trans.
Pf05014; Nuc_decxyrib_trins.
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25-OCT-2004 (Rel. 45, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Nucleoside deoxyribosyltransferase (EC 2.4.2.6)
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SEQUENCE 159 AA; 18252 MW;
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                                      NUCLEOTIDE SEQUENCE
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Percent Similarity:
Best Local Similarity:
   NCBI_TaxID=1579
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Pred. No.:
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Q74LQ9;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
STRAIN=NCC 533;
PubMed=14983040; DOI=10.1073/pnas.0307327101;
PubMed=14983040; DOI=10.1073/pnas.0307327101;
Putter A.-C.; Zwahlen M.-C.; Rouvet M., Altermann E., Barrangou R., Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
The genome sequence of the probiotic intestinal bacterium
Lactobacillus johnsonii NCC 533 ";
Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).

I. FUNCTION: Catalyzes the cleavage of the glycosidic bond of 2'-
Cecxyribonucleosides and the transfer of the deoxyribosyl moiety
to an acceptor purine or pyrimidine base (By similarity).

C. -CATALYTIC ACTIVITY: 2-deoxy-D-ribosyl-base(1) + base(2) = 2-deoxy-
D-ribosyl-base(2) + base(1).

D-ribosyl-base(2) + base(1).

C. -- SIMILARITY: Belongs to the nucleoside deoxyribosyltransferase
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|AlaGlyTrpPheThrGluThrGlnAsnLysAlaTyrLysAspAlaMetSerAlaLeuAsn
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6CE8A86B0553152A CRC64;
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Pfam; PF05014; Nuc deoxyrib tr; 1.
Complete proteome; Nucleotide metabolism; Transferase.
ACT_SITE 90
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75.84%
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144 AspPheAsnLysProArgTyrAsnPheTyrAspGlyAlaValTyr
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                                                                           STANDARD;
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                                                                                                                                                                                                                     Lactobacillus fermentum
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                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
STRAIN-CIP 102980T;
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                                                                                                                                                                                                                                                                                 NCBI_TaxID=1613;
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MEDLINE-21012342; PubMed=11129605; DOI=10.1271/bbb.64.2243;
A Okuyama K., Neguchi T.;
Okuyama K., Neguchi T.;
Okuyama K., Neguchi T.;
Okuyama K., Neguchi T.;
Indexyribosyltransferase-II gene from Lactobacillus helveticus.";
Blosci, Blosci, Blotechnol. Blochem. 64:2243-2245(2000).
REMBL, AB019914; BAA92683.2; -; Genomic_DNA.
R PIR; JC7522; JC7522.
R RSSP; Q9RSV5; 1F8Y.
R RSP; Q9RSV5; 1F8Y.
R GO; GO:0016740; Fitransferase activity; IEA.
R InterPro; IPR007710; N deoxyrib_trans.
R Pfam; PF05014; Nuc_deoxyrib_tr; 1.
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Nucleoside deoxyribosyltransferase-II
                                                                                            PRT;
                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 AA; 18318 MW;
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634.00
87.10%
72.90%
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                                                                                          Q9KWF0 LACHE PRELIMINARY;
Q9KWF0;
                                                                                                                                                                                                                         Lactobacillus helveticus
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Best Local Similarity:
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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-1- FUNCTION: Catalyzes the cleavage of the glycosidic bond of 2'-
deoxyribonucleosides and the transfer of the deoxyribonsyl moiety
to an acceptor purine or pyrimidine base (By similarity).

-1- CATALYTIC ACTIVITY: 2-deoxy-D-ribosyl-base(1) + base(2) = 2-deoxy-
D-ribosyl-base(2) + base(1).

-1- PATHWAY: Nucleotide metabolism.
-1- SIMILARITY: Belongs to the nucleoside deoxyribosyltransferase
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Lactobacillus.
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                                                   25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Nucleoside deoxyribosyltransferase (EC 2.4.2.6)
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InterPro; IPR007710; N_deoxyrib_trans.
Pfam; PF05014; Nuc deoxyrib_tr; 1.
Nucleotide metabollsm; Transferase.
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SEQUENCE 168 AA; 18896 MW; 362162F43586
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STRAIN-NCFM;

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A pubmed-15671160; DOI=10.1073/pnas.0409188102;

A Altermann B., Russell W.M., Azcarate-Peril M.A., Barrangou R.,

A Altermann B., Russell W.M., Azcarate-Peril M.A., Barrangou R.,

A Altermann B., Russell W.M., Azcarate-Peril M.A., Barrangou R.,

A Lick S., Hamrick A., Cano R., Klaenhammer T.R.;

Lick S., Hamrick A., Cano R., Klaenhammer T.R.;

Lactobacillus acidophilus NCFM.",

Proc. Natl. Acad. Sci. U.S.A. 102:3906-3912 (2005).

REMBL; CP000033; AAV43441.1; -; Ganomic_DNA.

RO, GO.0016740; Firansferase accivity; IEA.

InterPro; IPR007710; N_deoxyrib_trans.

Ream; PP05014; Nuc_deoxyrib_trans.

Ream; PP05014; Nuc_deoxyrib_tri.

Ream; PR05014; Nuc_deoxyrib_tri.

SEQUENCE 167 AA; 18933 MW; A80408F06C3E4D98 CRC64;
                                                                                                                                                                                                                                                                     GAAGCCCTCAAGGAAAACCCAACGATTGACCTGGAAAACAGCTACGTTCCCCTGGACAAC 144
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                                                                                                                                           GACGAAGACTACGGCAAGCCGATCAACCTCATG---AGCTGGGGCGTCAGC-----
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140 AspGlyAsnThrGluPheGluLysLeuAlaAspTyrAsnPheAsnGlu 155
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Lactobacillus.
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10-MAY-2005 (TrEMBLrel. 30, Last i
Putative deoxyribosyltransferase.
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QSFINO;
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                                                                   CAAGGCAAG---TACGTCCTTTTGGTCATCCCGGACGAAGACTACGCCAAG---CCGATC 375
                                                                                                                                    110 LeuHisLysProlleValLeuLeuProPheThrLysLysAspLysSerAlaTyrGluAla 129
                                                                                                                                                                                                     ------AGCTGGGCGTCAGCGACAACGTGAAGATG 417
                                                                                                                                                                                                                                                              130 AsnieuMetieuAlaArgGlyValThrTrrp---LeuGluProAsn-----AspPhe 146
   LeuTyrAspMetAspGlnIleAspGluGlyIleCysMetGluIleGlyMetPheValAla 109
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AX104166; BAC01952.1; -; Genomic_DNA.
BMBL; AB076265; BAC00952.1; -; Genomic_DNA.
BDB; 1820; X-ray; A/B/C=1.167.
BDB; 1821; X-ray; A/B/C=1.167.
BDB; 1831; X-ray; A/B/C=1.167.
BDB; 1831; X-ray; A/B/C=1.167.
GO; GO:0050144; F:nucleoside deoxyribosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
InterPro; IPR007710; N deoxyrib_trans.
PFem; PF05014; Nuc_deoxyrib_trans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2005 (TrEMBLrel. 29, Last sequence update)
Purine trans deoxyribosylase (Nucleoside deoxyribosyltransferase-I)
(EC 2.4.2.6).
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Lactobacillus.
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SOUENCE 167 AA; 18713 MW; 5540581511CB4787
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Lactobacillus helveticus.
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                                         -----TCAAGGAAAACCCAACGATTGACCTGGAAAACGTTC 133
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Ser---ThrThrSerLysArgProThrHis-------GluThrThrThrThrThrSer
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                                                                                  76 ThrThrGluLysSerThrThrArgArgThrThrThrThrThrArgGlnThrThrThrArg
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EMBL, AF068065; AAC98153.1; -; Genomic_DNA.
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Bukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporididae; Cryptosporidium.
NCBI_raxID=5907;
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|GluLysLysMetAsnLeuMetIleAlaGlnGlyValThrThrIleIleAspGlyAsnThr 143
                                         GACAAGGTTTGGGCTACGCCACCTACAACAACGACTTGAACGGGATCAAGACCAACGAC 249
                                                                                                                         250 ATCATGCTGGGTGTCTACATCCCTGACGAAGAAGACGTCGGCCTGGGCATGGAACTGGGT 309
                                                                                                                                                                                                              TACGCCTTGAGCCAAGGCAAGTACGTCCTTTTGGTC-----ATCCCGGACGAAGACTAC 363
                                                                                                                                                                   84 CysGlyValPheLeuTyrAspMetAspAsnIleAspAspGlySerAlaPheGluIleGly 103
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                                                                                  83
                                                                 ------ValAspProGluGluLysAspProGluAlaAspGlyLeuArg
                                                                                                                                                                                                                                                                                               GGCAAGCCGATCAACCTCATG---AGCTGGGGCGTCAGC-----GACAACGTGATC
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MEDLINE=88332966; PubMed=3138416;
Martin C.H., Mayeda C.A., Meyerowitz E.M.;
"Evolution and expression of the Sgs-3 glue gene of Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosopila yakuba (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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C0C5246B482A261C CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
01-UUJ-2004 (Rel. 44, Last annotation update)
Salivary glue protein Sgs-3 precursor.
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FlyBase; FBgn0013172; Dyak\Sgs3
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ID SGS3_DRO
AC P13728;
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US-10-049-750-13 (1-483) x Q9VR49_DROME (1-1286)
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                                                                                                                                                                                                       260 GIGICIACAICCCIGACGAAGAGACGICGGCCIGGGCAIGGAACIGGGIIACGCCIIGA 319
                                                                                                                                                                                                                                                                                               :::|||::: ||||
435 ThrThrThrThrThrThrThrThrThr-------ThrThrThrThr 448
                                                                                                                                                                                                                                                                                                                                                                                              140 ACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAATACCTGCATGACAAGGTTT 199
                                                                                                      200 GGGCTACGGCCACCTACAACAACGACTTGAACGGGATCAAGACCAACGACATCATGCTGG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 GCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACTACGGCAAGCCGATCAACC
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Haxapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAACAAGCCGCGCTTCGACTTCTACGAAGGTGCCGTATACT 481
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Name=Sgs1; ORFNames=CG3047;
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin:
             Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Wassenbech J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu S., Zhu X., Smith H.O. The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                   Carlson J.W., Halpern A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berkeley Drosophila Genome Project, Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R., Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
Sun E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E. Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.: Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                      MUCLEOTIDE SEQUENCE.
MEDLINE=22426055; PubMed=12537568;
MEDLINE=22426055; PubMed=12537568;
MEDLINE=22426055; PubMed=12537568;
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., Pacorge R.A., Hoskins R.A., Laverty T., Muzny D.M., Nolson C.R., Pacleb J.M., Park S., Pefelfer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Printalning a whole-genome shotgum: release 3 of the Drosophila melanogaster euchromatic genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Annotation of the Drosophila melanogaster euchromatic genome:
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Biol. 3: RESEARCH0084.1-RESEARCH0084.20(2002)
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ACTAAATGCCAAAAAGACGATCTACTTCGGTGCCGGCTGGTTCACTGACCGCCAAAACA 64

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GAAGCCCTCAAGGAAAACCCAACGATTGACCTGGAAAACAGCTACGTTCCCCTGGACAAC 144
    245 ACGACATCATGCTGGGTGTCTACATCCCTGACGAAGAAGACGTCGGCCTGGGCATGGAAC 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ILL903;
MEDLINE=21253186; Pubmed=11337471; DOI=10.1101/gr.GR-1697R;
MEDLINE=21253186; Pubmed=11337471; DOI=10.1101/gr.GR-1697R;
Melosenbach J., Bhrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis spp. lactis ILL403.";
Genome Res. 11:731-753(2001):
EMBL; AE006284; AAK04591.1; -; Genomic_DNA.
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-----ThrAlaThrProThr-----AsnThrProThrProAlaProGluThr 582
                                                                                                                        125 GCTACGTTCCCCTGGACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCCGGAATACC
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11 ValTyrLeuAlaAlaProPhePheSerGluSerGlnIleLysLysValGluLeuLeuGlu
                                          ----TGGAAGCCCTCAAGGAAAACCCAACGATTGACCTGGAAAACA
                                                                             466 ThrThrThrThrThrLysProProThrThrThrThrThrThrThrThrThrThrThrThrThr
                                                                                                                                                                                                        185 TGCATGACAAGGTTTGGGCTACGGCCACCTACAACAACGACTTGAACGGGATCAAGACCA
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ThrThrThrThrThrThrThrThrThrSerThrLys------------------
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 17, Last annotation update)
Hypothetical protein yejD.
Name=yejD; OrderedLocusNames=LL0493;
Lactooccus lactis (subsp. lactis) (Streptococcus lactis)
Bacteria; Firmicutes; Lactobacillales; Streptococcaees; Lactooccus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425 TGAAGGACTTCAACTTCAACAAGCCGCGCTTCGACTTCTACGAAGGTGCCGTATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       556 AlaAlaThrSerThrGlu---AlaProAlaGluProThrThr-------
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Pfam; PF05014; Nuc_deoxyrib_tr; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 159 AA; 18295 MW; 98BAE589D9C099C3
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Q9CI73;
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                                                               Ser------ArgProThrThrThrThrProArgSerThrThrThr 246
                                                                                                                                          247 ThrThrSerArgProThrThrThrThrProArgSerThrThrThrThrThrThrArgArg 266
                                                                                                                                                                                                        217
                                                                                                                                                                                                                                                                                                             ---ThrThr 350
                                                                                                                                                                                                                                           267 ProThrThrThrProArgCysThrThrThrThrSerThrCysAlaProThrThr 286
                                                                                                                                                                                                                                                                                                                                                                   TGGGTGTCTACATCCCTGACGAAGAAGACGTCGGCCTGGGCATGGAACTGGGTTACGCCT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAGCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACTACGGCAAGCCGATCA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCTCATGAGCTGGGGGGTCAGCGACAACGTGATCAAGATGAGCCAGCTGAAGGACTTCA 436
ThrProCysThrCysAlaGlnThrThrThrThrProArgSerThrThrThrThrThrSerThr 232
                                                                                                                     125 GCTACGTTC---CCCTGGACAACCAGTACAAGGGTATCCGGGTTGATGAACACCCGGAAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTACTTCGGTGCCGGCTGGTTCACTGACCGCCAAAACAAAGCCTACAAGGAAGCCA--- 82
                                                                                                                                                                                                                                                                                                                                                                                           307 ThrThrThrThsSerThrCysSerProThrArg------ThrThrPro
                                                                                                                                                                                                     ----ACCTGCATGACAAGGTTTGGGCTACGGCCACCTACA-----
                                                                                                                                                                                                                                                                                     -----ACAACGACTTGAACGGGATCAAGACCAACGACATCA-----TGC
                                        AAGCCTACAAGGAAGCCATGGAAGCCCTCAAGGAAAACCCAACGATTGACCTGGAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBL_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J., Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Nell S., Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.(Submitted (UNI-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, CT005251; CAJ02899.1; -; Genomic_DNA.
InterPro; IPR007099; LRR.
InterPro; IPR007099; LRR.
PF00560; LRR_1; 6.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Surface antigen protein 2, putative.
ORFNames=LmjF12.0830;
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SEQUENCE 648 AA; 68470 MW;
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Q4QGJ2;
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| AspileileValAlaileValAspPheAspHisGlnAspThrAspSerGlyThrAlaTrp 100
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GluLeuGlyTyrAlaIleAlaLeuGluLysProThrTyrLeuIleArgPheGluAspThr 120
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                                                                                                                                                                    ---TGGGCTACGGCCACCTACAACAACGACTTGAACGGGATCAAGACCAAC 246
                                                                                                                                                                                                                                                                 GACATCATGCTGGGTGTCTACATCCCTGACGAAGAAGACGTC-----GGCCTGGGCATG 300
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    ||||||| :::||| |||::: ||| || AsnAlaLeuSerLysAsnLysThrVal-----AlaAsnPhePheSerProMetArgCys 48
                                                                                                 GAACTGGGTTACGCCTTGAGCCAAGGCAAGTACGTCCTTTTGGTCATCCCGGACGAAGAC
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Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
NCBI_TaxID=237631;
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Q4P695 USTWA PRELIMINARY;
Q4P695;
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Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C., Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P., Rutman M., Schupbach R., Seaman C., Settipalli S., Sharper T., Sharper J., Sharper T., Spercer B., Stalker J., Smirnov S., Smith C., Sougnez C., Spencer B., Stalker J., Stange-thomann N., Stavropoulos S., Stetson K., Stone C., Stubbs M., Talamas J., Tchuinga P., Tenzing P., Tesday S., Theodore J., Thoulutsang Y., Topham K., A. Towey S., Tsamla T., Tsomo N., Vallee D., Vassliev H., Wenkstaraman V., Vinson J., Vo A., Made C., Wang S., Wangchuk T., Wenkstaraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T., Amangdi T., Whitekner C., Wilkinson J., Wu Y., Wyman D., Yadav S., Zimmer A., Zody M., Lander E., The genome sequence of Ustilago maydis.", The genome sequence of Ustilago maydis.", L. CAUTION: The sequence shown here is derived from an EMBL/Genbank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 TTGACCTGGAAAACAGCTACGTTCCCCTGGACAACCAGTACAAGGGTATCCGGGTTGATG 169
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10-MXY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Secreted protein with cysteine rich repeats and a mucin like threonine rich repeat, signal peptide, transcripts identified by EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 ArgserserthrthrserTyrserThrSerserSerSerThrAsnArgAlaLeuThrthr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AACF01000154; EAK85643.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 716 AA; 76918 MW; COA3C76508C98321 CRC64;
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Mismatches:
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Matches:
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QSCVM4;
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ORFNames=cgd8_3520;
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGCCCTCAAGGAAAACCCAACGATTGACCTGGAAAACAGCTACGTTCCCCTGGACAACC 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 GCAAGTACGTCCTTTTGGTCATCCCGGACGAAGACTACGGCAAGCCGATCAACCTCATGA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 ProThrThrThrThrThrArgProThrThrThrThrThrThrThrThrThrThrThr 961
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                                                          [1]

WUCLEOTIDE SEQUENCE.

STRAIN-IOWA type II;

PubMed=15044751; DOI=10.1126/science.1094786;

Abrahamsen M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu G.,

Lancto C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,

Bankier A.T., Dear P.H., Konffortov B.A., Spriggs H.F., Iyer L.,

Anantharaman V., Aravind L., Kapur V.;

"Complete genome sequence of the apicomplexan, Cryptosporidium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGCCACCTACAACAACGACTTGAACGGGATCAAGACCAACGACATCATGCTGGGTGTCT
                                                                                                                                                                                                   parvum.";
Science 304:441-445(2004).
Science 304:441-445(2004).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR010503; LT-IIB.
InterPro; IPR000429; Prot inh hirudin.
InterPro; IPR000783; NApol RPBS.
InterPro; IPR009032; Vpu cyl.
SEQUENCE 1124 AA; 120832 MW; E3EB73E8DC34C87E CRC64;
              Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida,
Cryptosporidiidae, Cryptosporidium.
OCDI_TaxID=5807;
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Matches:
Conservative:
Mismatches:
Indels:
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InterPro; IPR000074; ApoAl A4 E.
InterPro; IPR010380; Cyt c b562.
InterPro; IPR011992; BF-Hand type.
InterPro; IPR02563; Flv red_FWW_bind.
InterPro; IPR004281; IL12.
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136.50
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Cryptosporidium parvum.
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Best Local Similarity:
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Search completed: December 23, 2005, 22:42:39 Job time : 137.382 secs

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December 23, 2005, 21:47:05; Search time 188 Seconds (without alignments) 366.928 Million cell updates/sec
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1 MPKKTIYFGAGWFTDRQNKA......QLKDFNFNKPRFDFYBGAVY 157
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2001s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query	Query Match Length DB	DB	ΙD	Description
-	848	100.0	157	4	AAB67589	Aab67589 Amino aci
7	842	99.3	157	œ	ADR97103	Adr97103 N-deoxyri
٣	728	85.8	158	9	ABP98175	Abp98175 Amino aci
4	719	84.8	159	9	ABP98180	Abp98180 Amino aci
S	637	75.1	158	2	AAG66170	Aag66170 L. helvet
9	629	74.2	133	9	ABP98179	Abp98179 Amino aci
7	405	47.8	84	9	ABP98178	Abp98178 Amino aci
80	209	24.6	168	9	ABP98177	Abp98177 Amino aci
σ	166.5	19.6	167	9	ABP98176	Abp98176 Amino aci
10	136.5	16.1	159	ß	ABB53802	Abb53802 Lactococc
11	96	11.3	1149	ß	ABB77620	Abb77620 AmEPV P4a
12	94	11.1	750	-	AAP82940	Aap82940 Atrial na
13	91.5	10.8	156	7	ADC96860	Adc96860 E. faeciu
14	91	10.7	719	σ	ADW47705	Adw47705 F. magna
15	86.5	10.2	462	Ŋ	ABB54050	Abb54050 Lactococc
16	85.5	10.1	438	4	AAB95642	Aab95642 Human pro
17	85.5	10.1	456	œ	ADH41469	Adh41469 Novel hum
18	85.5	10.1	464	m	AAB23624	
19	85.5	10.1	487	œ	ADH41499	Adh41499 Novel hum
20	85.5	10.1	487	œ	ADH41497	Adh41497 Novel hum
21	•	10.1	487	œ	ADH41493	Adh41493 Novel hum
22	85.5	10.1		œ	ADH41495	Adh41495 Novel hum
23	85.5	10.1	487	89	ADH41463	Adh41463 Novel hum
24	85.5	10.1	487	89	ADS88243	Ads88243 Human pro

Adh41485 Novel hum	Adh41467 Novel hum	Aab90548 Human sec	_	Albumi	Adh41489 Novel hum	Adh41471 Novel hum	Adh41465 Novel hum	Novel	Adh41479 Novel hum	Aau08684 Human FCT	Aau08683 Human FCT	Human	Adb32035 Human FCT	Adh41491 Novel hum	Adh41473 Novel hum	Abo53100 Human put	Adx07993 Cyclin-de	Ade58906 Human Pro	Add45534 Human Pro	Ade61258 Human Pro
ADH41485	3 ADH41467	AAB90548	5 ABG65427	3 ADL78694	3 ADH41489	3 ADH41471	3 ADH41465	3 ADH41477	3 ADH41479	1 AAU08684	I AAU08683	/ ADB32033	7 ADB32035	3 ADH41491	3 ADH41473	5 ABO53100	) ADX07993	7 ADE58906	7 ADD45534	/ ADE61258
243 E	247 8	396	396	396	452 8	456	456	456 E	456 E	487 4	487 4	487 7	487	487	493 8	706	1042	1046	1046	1046
10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.0	9.9	6.6	6.6	6.6	6.6
84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84	84	84	84	84
22	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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The present sequence represents a nucleoside 2-deoxyribosyltransferase enzyme. This enzyme is involved in the biosynthesis of deoxyribonucleosides, and is used in the method of the invention. The specification describes a method for the in vitro enzymatic synthesis of deoxyribonucleosides. The method comprises reacting deoxyribose 1-phosphate and a nucleobase to form a deoxyribonucleoside and an inorganic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          In vitro enzymatic synthesis of deoxyribonucleosides comprises reacting deoxyribose 1-phosphate and a nucleobase to form a deoxyribonucleoside and an inorganic phosphate.
                                                                                                                                            Deoxyribonucleoside; deoxyribose 1-phosphate; thymidine phosphorylase; purine nucleoside phosphorylase; phosphopencose mutase; phosphopencose aldolase; fructose 1.6-diphosphate aldolase; deoxyriboxinase; deoxyriboxyriboxinase; nucleoside 2-deoxyribosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                               Amino acid sequence of a nucleoside 2-deoxyribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ihlenfeldt H, Barzu O, Sakamoto H, Pistotnik
Pochet S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 62-63; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            (HOFF ) ROCHE DIAGNOSTICS GMBH.
(INSP ) INST PASTEUR.
(PHAR-) PHARMA-WALDHOF GMBH & CO KG.
               AAB67589 standard; protein; 157 AA
                                                                                                                                                                                                                                                                                                                               18-AUG-2000; 2000WO-EP008088.
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                                                                                 (first entry)
                                                                                                                                                                                                                              Lactobacillus leichmannii.
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N-PSDB; AAF55445.
                                                                                                                                                                                                                                                               WO200114566-A2.
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                                                                               29-MAY-2001
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                                                AAB67589;
AAB67589
ID AAB6
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                                                                                                                                                                                                                 DKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALGYALGQKYVLLVIPDEDYGK 120
                                                                                                                                                                                                  DKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGK 120
phosphate. Enzymes which may be used in the method of the invention include thymidine phosphorylase, purine unclosside phosphorylase, phosphopentoes aldolase, fructose 1,6-diphosphate aldolase, deoxyribokinase, and nucleoside 2-deoxyribosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; antimicrobial; N-dideoxyribosyltransferase; DDTP; N-deoxyribosyltransferase; DTP; antitumour; infection; ddC; ddI; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            particularly for evolving an N-deoxyribosyltransferase to produce an N-dideoxyribosyltransferase for preparation of antitumor nucleosides and
                                                                                                                                                              MPKKTI Y FGAGWFTDRQNKAYKEAMEALKENPTI DLENSYVPLDNQYKGI RVDEHPEYLH
                                                                                                                                             1 MPKKTIYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLH
                                                                                                                     Gaps
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                                                                                          Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins to modify characteristics,
                                                                                                                                                                                                                                                                                                                                                                                                                          N-deoxyribosyltransferase (DTP) with G9S mutant, seq id 1.
                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild-type Gly replaced with Ser"
                                                                                                                                                                                                                                                   PINLMSWGVSDNVIKMSQLKDFNFNKPRFDFYEGAVY 157
                                                                                                                                                                                                                                                                    PINLMSWGVSDNVIKMSQLKDFNFNKPRFDFYEGAVY 157
                                                                                          100.0%; Score 848; DB 4; 100.0%; Pred. No. 5.8e-84;
                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; SEQ ID NO 2; 51pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                Ź
                                                                                                                                                                                                                                                                                                                                               ADR97103 standard; protein; 157
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CENT NAT RECH SCI
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                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactobacillus leichmannii
                                                                                                                    Matches 157; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-693069/68.
                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                 Sequence 157 AA
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(CNRS ) CNRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaminski PA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                         ADR97103;
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                                                                                                                                                                                                                                                     121
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                                                                                           Query Match
                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                     61 DKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGK 120
                                                                                                                                                                                                                                                                                                                                                    DKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGK 120
             dideoxyribosyltransferase (DDTP), i.e. an eizyme able to transfer dideoxyribose from one dideoxyribonucleotide to another. Such an enzyme is used for preparation of nucleotides and nucleosides that have antitumour activity or can be used to treat infections, particularly ddc and ddl. The current sequence represents the N-deoxyribosyltransferase (DTP) amino acid sequence containing a G9S mutation. This protein displays the activity of N-dideoxyribosyltransferase.
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specifically used to evolve an N-deoxyribosyltransferase (DTP) to an N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preparing
                                                                                                                                                                                                                                                                             1 MPKKTIYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLH
                                                                                                                                                                                                                                                                                                    MPKKTIYFSAGWFTDRQNKAYKEAMBALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-deoxyribosyltransferase; ntd gene; enzyme; antitumour chemotherapy; deoxyribonucleotide synthesis; infection; insecticide; herbicide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                       Length 157;
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                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PINLMSWGVSDNVIKMSQLKDFNFNKPRFDFYEGAVY 157
                                                                                                                                                                                                                                                                                                                                                                                                                           121 PINLMSWGVSDNVIKMSQLKDFNFNKPRFDFYEGAVY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quenee P,
                                                                                                                                                                                                     99.3%; Score 842; DB 8; 99.4%; Pred. No. 2.6e-83;
                                                                                                                                                                                                                                         0; Mismatches
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(NARE-) INST NAT RECH AGRONOMIQUE
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N-PSDB; ACC43580, ACC43586.
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                                                                                                                                                                                                                                         Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactobacillus helveticus
                                                                                                                                                                                                                        Similarity
                                                                                                                                                                  Sequence 157 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003025163-A2.
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ABP98175
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The invention relates to a method for evolution of a protein (X) so a modify its characteristics. Further disclosed are mutated proteins (X: produced by the new method and with altered activity, relative to (X) Also disclosed is a nucleic acid (I) comprising a sequence for N-dideoxyribosyltransferase (DDTP), obtained from an N-deoxyribosyltransferase (DDTP), using the new method. The method is

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Lactobacillus helveticus.
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Matches 114; Conservative
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                                                                                                                                                                                                                                                                                RESULT S
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                                                                                                                                                                                                                                        VWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPI 122
                                                                                                                                                                                                                                                          preparing
related
                                                                                                                                                      3 KKTIYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDK
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                                                                                                              Gaps
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                                                                    Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of N-deoxyribosyltransferase protein.
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quenee P,
                                                                  85.8%; Score 728; DB 6; Lv 82.6%; Pred. No. 7.3e-71; ive 20; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                124 NLMSWGVCDNAIKISELKDFDFNKPRYNFYDGAVY 158
                                                                                                                                                                                                                                                                                                                            NLMSWGVSDNVIKMSQLKDFNFNKPRFDFYEGAVY 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New N-deoxyribosyltransferase from deoxyribonucleotides, e.g. for use nucleic acid and antibodies.
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(NARE-) INST NAT RECH AGRONOMIQUE.
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                                                                                                              Conservative
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Matches 128; Conserv
                                                                                      Local Similarity
les 128; Conser
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                            Sequence 158
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                                                                    Query Match
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Matches
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4 KTIYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDKV 63

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                        63 VWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 EWASATYHNDLVGIKTSDVILGVYLPQEEHVGLGMELGYPLSQGKLFFWFSHMKDYGKPI 123
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WATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleoside deoxyribosyltransferase-II; enzyme; deoxynucleoside; drug;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L. helveticus nucleoside deoxyribosyltransferase-II.
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73.5%; Pred. No. 6.2e-61;
iive 21; Mismatches 20;
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                                                                                                                                             124 LMSWGVSDNVIKMSQLKDFNFNKPRFDFYEGAVY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enzymatic preparation of deoxynucleoside.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 10; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                    AAG66170 standard; protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-AUG-2000; 2000JP-00239443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-AUG-2000; 2000JP-00239443.
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ABP98179
ID ABP9
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ABP98179;

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The present sequence represents a N-deoxyribosyltransferase protein from lactobacillus. The enzyme is encoded by the ntd gene. The N-deoxyribosyltransferase protein is useful to raise specific antibodies, and for in vitro or in vivo enzymatic synthesis of deoxyribonucleotides, particularly those containing non-natural bases. These deoxyribonucleotides are useful for treating bacterial, viral (e.g. HIV), parasitic or fungal infections, for antitumour chemotherapy, and as insecticides or herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 NQYKGIRVDEHPEYLHDKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NQYKGIRVDEHPEYLHDIEWASATYHNDLVGIKSSDIMLGVYLPEEEDVGLGMELGYALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-deoxyribosyltransferase; ntd gene; enzyme; antitumour chemotherapy; deoxyribonucleotide synthesis; infection; insecticide; herbicide.
deoxyribonucleotide synthesis; infection; insecticide; herbicide
                                                                                                                                                                                                                                                                                                                                                                                      New N-deoxyribosyltransferase from Lactobacillus, useful for deoxyribonucleotides, e.g. for use as antiviral agents, also nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of N-deoxyribosyltransferase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 405; DB 6; L
Pred. No. 5.1e-36;
8; Mismatches 3;
                                                                                                                                                                                                                                                                                          Quenee P,
                                                                                                                                                                                                                                                                                          Marliere P,
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                                                                                                                                                                                                                                                    AGRONOMIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP98177 standard; protein; 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 65; 70pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-2001; 2001FR-00011911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2002; 2002WO-FR003120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 47.8%;
Local Similarity 86.9%;
Nes 73; Conservative
                                                                                                                                                        12-SEP-2002; 2002WO-FR003120
                                                                                                                                                                                            14-SEP-2001; 2001FR-00011911
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                                                                                                                                                                                                                                                                                        Tailliez P,
                                      Lactobacillus crispatus
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                                                                                                                                                                                                                                PASTEUR.
NAT RECH
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                                                                                                                                                                                                                                                                                                                                                N-PSDB; ACC43583
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                                                                            WO2003025163-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 84 AA;
                                                                                                                                                                                                                                  (INSP ) INST
(NARE-) INST
                                                                                                                                                                                                                                                                                          Kaminski P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-AUG-2003
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VYLPEEEDVGLGMELGYALSQGKYILLVIPDEDYGKPINLMSWGVCDNVIKISELKDFDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VXIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPINLMSWGVSDNVIKMSQLKDFNP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEALKKNPIVDLENSYVPLDNQYKGIRVDEHPEYLHDIEWASSIYHNDLVGIKSSDVMLG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
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related
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                                                                                                                                    N-deoxyribosyltransferase; ntd gene; enzyme; antitumour chemotherapy; deoxyribonucleotide synthesis; infection; insecticide; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-deoxyribosyltransferase; ntd gene; enzyme; antitumour chemotherapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New N-deoxyribosyltransferase from Lactobacillus, useful for deoxyribonucleotides, e.g. for use as antiviral agents, also nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cotaya R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 133;
                                                                                              Amino acid sequence of N-deoxyribosyltransferase protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quenee P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.2%; Score 629; DB 6; 84.2%; Pred. No. 3.6e-60; ive 17; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                              Marliere P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP98178 standard; protein; 84 AA.
                                                                                                                                                                                                                                                                                                                                                                                    (INSP ) INST PASTEUR.
(NARE-) INST NAT RECH AGRONOMIQUE.
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NRPRFNFYDGAVY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKPRFDFYEGAVY 157
                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112, Conservative
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                                                                                                                                                                                          Lactobacillus amylovorus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 133 AA;
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                                                          11-AUG-2003
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Query Match Best Local (

Matches

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ABP98178

ABP98178
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0; Gaps

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Length 84;

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Cotaya

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ABB53802 standard; protein; 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus lactis; IL1403
                                                                                                                                                                                                                                                                  49; Conservative
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                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                            Sequence 167 AA;
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16-MAY-2002
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                                                                                                                                                                                                                                                               .g. HIV),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 ATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGK-YVLLVIPDEDYGK-PI 122
                                                                                                                                                                                           The present sequence represents a N-deoxyribosyltransferase protein from lactobacillus. The enzyme is encoded by the ntd gene. The N-deoxyribosyltransferase protein is useful to raise specific antibodies, and for in vitro or in vivo enzymatic synthesis of deoxyribonucleotides, particularly those containing non-natural bases. These deoxyribonucleotides are useful for treating bacterial, viral (e.g. HIV), parastic or fungal infections, for antitumour chemotherapy, and as insecticides or herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                          New N-deoxyribosyltransferase from Lactobacillus, useful for preparing deoxyribonucleotides, e.g. for use as antiviral agents, also related nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                          12 IYLATSFRNEEQRARIPQALAQLEANPTVGVVHQ--PFDFQYKDARVDSDPAGVFGSLEW
                                                                                                                                                                                                                                                                                                                                                                                                          6 IYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDKV-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-deoxyribosyltransferase; ptd gene; enzyme; antitumour chemotherapy; deoxyribonucleotide synthesis; infection; insecticide; herbicide.
                                                                                                                                                                                                                                                                                                                                                    24.6%; Score 209; DB 6; Length 168; 36.4%; Pred. No. 3.4e-14;
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                                          Cotaya R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of N-deoxyribosyltransferase protein.
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                   59;
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                                          Quenee P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLM-----SWGVSDNVIKMSQLKDFNFNKP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 NLMLARGVTTW-LEPN--DFSPLKDFNFNHP 157
                                                                                                                                                                                                                                                                                                                                                               36.4%; Pred. ...
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                                        Marliere P,
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(INSP ) INST PASTEUR.
(NARE-) INST NAT RECH AGRONOMIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP98176 standard; protein; 167
                                                                                                                                                                   Claim 1; Page 64; 70pp; French
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                                        Tailliez P,
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 36.4 tes 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-313351/30.
N-PSDB; ACC43581.
                                                                   WPI; 2003-313351/30.
N-PSDB; ACC43582.
                                                                                                                                                                                                                                                                                                                           Sequence 168 AA;
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(NARE-) INST
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                                        Kaminski P,
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Matches
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The present invention is related to a Lactococcus lactis nucleotide sequence (ABA30521) and related proteins (ABB3300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHDKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLV---IP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a N-deoxyribosyltransferase protein from Lactobacillus. The enzyme is encoded by the ptd gene. The N-deoxyribosyltransferase protein is useful to raise specific antibodies, and for in vitro or in vivo enzymatic synthesis of deoxyribonuclectides, particularly those containing non-natural bases. These deoxyribonuclectides are useful for treating bacterial, viral (e.g. HIV), parasitic or fungal infections, for antitumour chemotherapy, and as insecticides or herbicides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
New N-deoxyribosyltransferase from Lactobacillus, useful for preparing deoxyribonucleotides, e.g. for use as antiviral agents, also related nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPKKTIYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::: | :||| : ||: ||: |
EKE--KKMNLMIAQGVTTIIDGNTEFEKLADYNFNECPFNPVRG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEDYGKPINLM-SWGVS---DNVIKMSQLKDFNFNKPRFDFYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.6%; Score 166.5; DB 6
29.9%; Pred. No. 1.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; SEQ ID NO 504; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Renault P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ź
                                                                                                                                                               Claim 1; Page 62-63; 70pp; French.
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or in vivo. The vector is useful for the delivery and expression of biologically useful proteins in gene therapy protocols, and for delivering large DNA segments for engineering of vertebrate cells. Polymucleotides of the invention have applications in techniques such as their use as insertion sites for foreign genes of interest, hybridisation probes, for chromosome and gene mapphing, in PCR technologies, and in the production of sense or antisense nucleic acids. Vectors of the invention provide for stable integration and expression of heterologous DNA in host cells, and are adapted for accepting large heterologous polymucleotide inserts which can be delivered in an infected or transformed cell and expressed in a stable fraction. The current sequence represents an amsacta moorei entomopoxvirus (AmEPV) P4a core protein (AMV139)

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7:
                                                                                                                                                                                                                              61 FTPEWAKATMENDVNEVNKADIIVAIVDFDHQDTDSGTAWELGYAIALEKPTYLIRFEDT 120
 biodegradation of a composition of interest. The invention helps research
                                                                                                                                                                                                               ----WATATYNNDLNGIKTNDIMLGVYIPDEEDV--GLGMELGYALSQGKYVLLVIPDED 117
                                                                                                                                                                                         9
        in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent wO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                               6 IYPGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDKV--
                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy, viral vector; chromosome mapping; gene mapping; deficiency disorder; P4a core protein.
                                                                                                                                           27;
                                                                                                                   Length 159;
                                                                                                                                         57; Indels
                                                                                                                                                                                                                                                             118 YGKPINLMSWGVSDN----VIKMSQLKDFNFNKPRFDFYEG 154
                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                  16.1%; Score 136.5; DB 5
26.7%; Pred. No. 2.6e-06;
iive 34; Mismatches 57
                                                                                                                                                                                                                                                                                                                                              ABB77620 standard; protein; 1149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   AmEPV P4a core protein (AMV139)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amsacta moorei entomopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-AUG-2001; 2001WO-US025287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-AUG-2000; 2000US-0224479P.
14-SEP-2000; 2000US-00662254.
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                         43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYFL ) UNIV FLORIDA.
                                                                                                                              Local Similarity
                                                                                            Sequence 159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200212526-A2
                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                    ABB77620;
                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic
                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                        RESULT 11
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PEYLHDKVWATATYNN-DL--NGIKTNDIMLGV-----YIPDEEDVGLGMELGYALSQ-- 105 

13 FTD--RQNKAYKEAMEALKENPTIDLEN--

12 26

44;

DB 5; Length 1149; 62; Indels

11.3%; Score 96; DB 23.7%; Pred. No. 1.2; ive 29; Mismatches

Local Similarity 23.74 les 42; Conservative

Matches

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Query Match

Sequence 1149 AA;

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Novel polypeptide, with diuretic action - is obtd. from atrium cardis of mammals showing specific bond to atrial natriuretic polypeptide and gene coding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          has diuretic (partic. natriuretic) and hypotensive action. See also AAN81690-93 and AAP81282-P81309. (Updated on 10-MAR-2003 to add missing
              Peptide specifically binds to atrial natriuretic polypeptide (ANP)
 ---GKYVLLV-IPDEDYG----KPINLMSWGVSDNVIKMSQLKDFNFNKPRFDFY
                                                                                                                                                                                         Diuretic; atrium cardis; atrial natriuretic peptide binding;
                                                                                                                                                                   Atrial natriuretic polypeptide binding polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page ?; 23pp; Japanese.
                                                                                  Ą.
                                                                                  AAP82940 standard; protein; 750
                                                                                                                                                                                                                                                                                                   86JP-00222192
                                                                                                                                                                                                                                                                                                                         86JP-00222192
                                                                                                                               (revised)
(first entry)
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                                                                                                                                                                                                       hypotensive action.
                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAN81690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 750 AA;
                                                                                                                                                                                                                                                   JP63079598-A
                                                                                                                                                                                                                                                                                                   22-SEP-1986;
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                                                                                                                               10-MAR-2003
23-NOV-1990
                                                                                                                                                                                                                                                                           09-APR-1988
                                                                                                         AAP82940;
 106
                                                                                                                                                                                                                             Mammalia.
                                                          RESULT 12
                                                                       AAP82940
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The invention relates to a recombinant entomopox virus (BPV) vector, comprising a polymucleotide encoding a protein operably linked with a heterologous promoter sequence. The invention also concerns methods for providing gene therapy for genetic deficiency disorders. Vectors of the invention are useful for delivering a polymucleotide encoding a protein call. The vector is introduced into the vertebrate cell preferably amammalian call, such as a human call. The vector is introduced into the vertebrate cell by infection in a viral particle, or by transfection, transduction, or injection either in vitro

Novel recombinant entomopox virus vector useful for delivering polynucleotide encoding protein to vertebrate cell, comprises polynucleotide encoding protein operably linked with heterologous

Moyer RW, Li Y, Bawden AL;

WPI; 2002-227161/28. N-PSDB; ABL56223.

Claim 75; Page 279-284; 326pp; English.

promoter sequence

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10;
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                                                                                             272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Entertrocceus faccium encoding an Entercocceus faccium polypebtide having one of 10 fully defined sequences given in the (or comprising 40 esquential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acid are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions resulting from E. faccium bacterial infection (e.g. urinary tract infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The
                                                                                                                                                                                                                           384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid derived from Enterococcus faecium encoding a
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                1 MPKKTIYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEH----
                                                                                             26 LPSRDYYECTG-----IYKEACTAY-----VDFMISVAKLIRQEKGLPVDENQLSLE
                                                                                                                              -----PEYLHDKVWATATYNN---DLNGIK-----TNDIM-
                                                                                                                                                            273 MNKVMELEKEIANATTKSEDRNDPMLLYNKMTLAQIQNNFSLEINGKSFSWSNFTNEIMS
                                                                                                                                                                                            -LGVYIPDEEDVGLGMELGYA---LSQGKYVLLVIPDEDYGKPINLMSWG-VSDNVIKMS
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine, urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
                               64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid derived from
1; Length 750;
                               48; Indels
11.1%; Score 94; DB 1
26.5%; Pred. No. 1;
ive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 6487; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B. faecium protein sequence SEQ ID 6487
                                                                                                                                                                                                                                                                                                                                                                         ADC96860 standard; protein; 156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-) GENOME THERAPEUTICS CORP.
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 Query Match
Best Local Similarity 26.5
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-799836/75.
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                                                                                                                                                                                                                                                                                          R 385
                                                                                                                                                                                                                                                             Q 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6583275-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1998;
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nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccinies contraining the nucleic acid are useful for preventing or treating Enterococcus faccium infections. The present sequence represents one if the disclosed E. faccium proteins.
                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying immunogenic protein useful as antigen in vaccine composition, involves obtaining protein complex comprising immunoglobulin or immunoglobulin-containing fraction from subject and identifying protein
                                                                                                                                                                                                                                                                                                      66 TATYNNDLNGIKTNDIMLGVYIPDEE--DVGLGMELGYALSQGKYVLLVIPDEDYGKPIN 123
                                                                                                                                                                                                                                65
                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                             14 IYLAGPFFSEEQIDRVSRIEKALEENKTV--TSFYSPRHYQ------ESNYELFSAGWA
                                                                                                                                                                                                                              6 IYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDKVWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunogenicity; immune disorder; cystic fibrosis; infection; cancer; neoplasm; respiratory disorder; antibacterial; cytostatic; immunosuppressive; cns-gen.; respiratory-gen.; immunoglobulin.
                                                                                                                                                                                           15;
                                                                                                                                                       7; Length 156;
                                                                                                                                                                                          74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROT-) PROTEOME SYSTEMS INTELLECTUAL PROPERTY P.
                                                                                                                                                                                                                                                                                                                                                                                                         | | : ::::: | | LITQSLHTYLKSDQAVREYDFETLPVETYVG 153
                                                                                                                                                                                                                                                                                                                                                                                  124 LMSWGVSDNVIKMSQ-LKDFNFNKPRFDFYEG 154
                                                                                                                                                       <u>D</u>3
                                                                                                                                                       10.8%; Score 91.5; Di 23.0%; Pred. No. 0.2;
                                                                                                                                                                                           28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 3; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weinberger R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADW47705 standard; protein; 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUN-2004; 2004WO-AU000856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUN-2003; 2003AU-00903317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                           35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F. magna protein L.
                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Finegoldia magna
                                                                                                                    Sequence 156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2005001480-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-2005
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                                                                                                                                                        YLHDKVWATATYNNDL----NGIKTNDIML---GVYIPDEEDVGLGMELGYALSQGKYV 109
                                                                                                                                      57
                                                                                                        Gaps
present sequence represents the amino acid sequence of the {\mathbb F}. magna antibody light chain binding protein, protein {\mathbb L}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleotide sequence useful in the identification or Lactococcus lactis and related species.
                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                   GWFTDRQNKAYKEAMEALKENP--TIDLENSYVPLDNQYKGIRVDEHPE
                                                                       10.7%; Score 91; DB 9; Length 719; ilarity 28.0%; Pred. No. 2.1; Conservative 17; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Renault P, Ehrlich SD;
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                                                                                                                                                                                                                                                                                                                                                             ABB54050 standard; protein; 462 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus lactis protein yheD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactococcus lactis; IL1403
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(first entry)
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                                                                                                                                                                                                                                                                                    ----PEETPEKP 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-043418/06.
                                                                    Query Match
Best Local Similarity
Matches 37; Conserv
                                           Sequence 719 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bolotine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FR2807446-A1
                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2003
16-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                           ABB54050;
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                                                                                                                                                                                                                                                                                     466
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Score 86.5; DB 5; Length 462; Pred. No. 3.4;

10.2%;

Query Match Best Local Similarity

Sequence 462 AA;

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                                                  218 FTLDQVMCFGDSENDLTMI-----SGVGYGIAMGNAVPEVKNIATYITDTN 263
                                                                                     58 YLHDKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDED 117
                             15 DRONKAYKEAMEALKENPTIDLENSY----VPLDNQYK-----GI-RVDEHPE 57
  Gaps
  51;
                                                                                                                                                            264 NQDGIAKALAYYG---LIHYSVEKDFVS----KDQNFNKVK-DFH 300
                                                                                                                                          -----YGKPINLMSWGVSDNVIKMSQLKDFNFNKPRFDFY 152
  Indels
 54;
 21; Mismatches
 Conservative
40;
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 Matches
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Search completed: December 23, 2005, 22:00:14 Job time : 191 secs

Sequence 69, Appl Sequence 65, Appl Sequence 73, Appl Sequence 73, Appl Sequence 1948, Ap Sequence 6783, Appl

Sequence 192, App Sequence 192, App Sequence 11595, A

Sequence 4391, Ap

Sequence 11595, A Sequence 99, Appl

ALIGNMENTS

Sequence 45, Appl Sequence 28646, A Sequence 7334, Ap Sequence 27095, A

Sequence 47, App]

US-09-535-008-69 US-09-535-008-65 US-09-535-008-73 US-09-535-008-73 US-09-134-001C-434 US-09-328-352-67434 US-09-422-936-47 US-09-422-936-47 US-09-422-936-47 US-09-422-936-47 US-09-422-936-47 US-09-422-931A-28646 US-09-422-931A-28646 US-09-370-838-192 US-09-107-532A-4391 US-09-370-838-192 US-09-864-133-192 US-09-816-11595 US-10-152-886-99

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Sequence 6487, Application US/09107532A; Patent No. 6583275; Patent No. 6583275; Patent No. 6583275; Patent No. 6583275; Patent No. 678276 No. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40, 489
REGISTRENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 6487:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature

: LOCATION: (B) LÖCATION 1...156

; SEQUENCE DESCRIPTION: SEQ ID NO: 6487:

US-09-107-532A-6487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: PC
OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
11659
11678
11679
1252
2522
308
8449
9644
992
1164
1164
633
653
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   \begin{array}{c} \mathbf{0} \\ \mathbf{
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72.5
72.5
72.5
   74
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73
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73
   Sequence 86, Appl
Sequence 28, Appl
Sequence 11, Appl
Sequence 17529, A
Sequence 17529, A
Sequence 17745, A
Sequence 4707, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 58, Appli
Sequence 58, Appli
Sequence 18446, A
Sequence 1852, Appli
Sequence 1846, A
Sequence 7, Appli
Sequence 7, Appli
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18005, A
30, Appl
67, Appl
2, Appli
4, Appli
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Sequence 75, Appl
Sequence 71, Appl
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                                                                                                                                                                                                                                            December 23, 2005, 21:56:48; Search time 47 Seconds (without alignments) 276.172 Million cell updates/sec
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848
1 MPKKTIYFGAGWFTDRQNKA......QLKDFNFNKPRFDFYEGAVY 157
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Sequence
Sequence
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( / cgn2_6/ptodata/1/iaa/5_COMB.pep:*
): / cgn2_6/ptodata/1/iaa/6_COMB.pep:*
): / cgn2_6/ptodata/1/iaa/H_COMB.pep:*
): / cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
): / cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
): / cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-618-919A-18
US-09-248-796A-18005
US-08-836-687B-30
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US-09-248-796A-17529
US-08-354-973-1
US-09-134-000C-4783
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US-09-134-001C-4707
US-08-795-475-3
US-08-325-278B-3
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US-09-299-268-58
US-09-248-796A-19446
US-09-107-532A-4152
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                              sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                  - protein search, using
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Maximum DB seq length: 2000000000
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Match Length DB
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76.5
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76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                  OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
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MEDIUM TYPE:
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                                                                                                                                                                                                       66 TATYNNDLNGIKTNDIMLGVYIPDEE--DVGLGMELGYALSQCKYVLLVIPDEDYGKPIN 123
                                                                                                                                                                                                                                   65 QEVYEKDMEELTNAEFVVAILDFEHQTIDPGTAYELGVATMLKKPMIIV---QEETVPTN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 WATATYNNDL------GLGMELGYAIPDEEDV------GLGMELGYALSQGK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 --SHNFSGDIALLELQHSIPLGPNVLPVCLPDNETLYRSGLLGYVSGFGMEMGMLTTELK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 GAGWFIDRONKAYKEAMEALKENPIIDLENSYVPLDNQYK-----GIRVDEHPEYLHDKV 63
                                                                                                               IYFGAGWFTDRONKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDKVWA
                                                                                                                                                       14 İYLAGPFFSEEQIDRVSRIEKALEENKTV--TSFYSPRHHQ------ESNYELFSAGWA
                                                                    Gaps
                  Query Match 10.8*; Score 91.5; DB 2; Length 156; Best Local Similarity 23.0*; Pred. No. 0.021; Matches 35; Conservative 28; Mismatches 74; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
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10.0%; Score 84.5; DB 2; Length 396;
Best Local Similarity 23.1%; Pred. No. 0.52;
Matches 30; Conservative 26; Mismatches 49; Indels 2:
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Sequence 28, Application US/08477451

Sequence 28, Application US/08477451

Patent No. 5928865

GENERAL INFORMATION:
APPLICANT: Covacci, Antonello
TITLE OF INVENTION: Helicobacter Pylori Cagi Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 86, Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:
JITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: PZO44P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 86
LENGTH: 396
                                                                                                                                                                                                                                                                                                 124 LMSWGVSDNVIKMSQ-LKDFNFNKPRFDFYEG 154
                                                                                                                                                                                                                                                                                                                           122 LMITQSLHTYLKSDQAVREYDFETLPVETYVG 153
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 ONKAYKEAMEALKENPTID--LENSYVPLDNQYKGIRVD-EHPEYLHDKVWATATYNNDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.8%; Score 83.5; DB 1; Length 382; Best Local Similarity 26.0%; Pred. No. 0.64; Matches 38; Conservative 22; Mismatches 71; Indels 1
                                                                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

FILING DATE:

ATORNEY/AGENT INFORMATION:

NAME: MCCLING, Barbara G.

REGISTRATION NUMBER: 33,113

REFERENCE/DOCKET NUMBER: 0335.002

TELEPHONE: 510-651-3542

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 382 amino acid

STRANDEDNESS: single
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TITLE OF INVENTION: Helicobacter Pylori Cagi Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 SDNVIKMSQLKDFNFNKPRFDFYEGA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 LDNIDYYLQLERNKFDSKAKDIAQKA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0335.002
                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08477451
Patent No. 5928865
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REPERENCE/DOCKET NUMBER: 03:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 11:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Emeryville STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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24 AMEALKENPT---IDLENSYVP-----LDNQYKGIRVD------EHPE 57
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9.7%; Score 82.5; Di
Best Local Similarity 22.6%; Pred. No. 3;
Matches 43; Conservative 26; Mismatches
                                                                                                                                                            117 DYGKPINLMSWGVSDNVIKMS--QLKD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : |::||
LLGYKFDEPR 682
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US-08-354-973-1
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                                                                                                                                                                                                                                                                                                                                                 99 ATTKDKAQALLQMGVPSLDEEQNKKASRLALSYKQA-----IEEYSNNISNLLSRKE 150
                                                                                                                                                                                                                                                                                                                        74 NGIKTND---IMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPI-NLMSWGV 129
                                                                                                                                                                                                                                                                     39 KSKAYGDLEQALKDNPLYKKILPNPYAYVINQETPTKEDKERLSYYPQVKTSSIFKKTT 98
                                                                                                                                                                                                                                            17 ONKAYKBAMEALKENPTID--LENSYVPLDNQYKGIRVD-EHPEYLHDKVWATATYNNDL 73
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                                                                                                                                                                                                       15;
                                                                                                                                                            ch 9.8%; Score 83.5; DB 1; Length 1781; Il Similarity 26.0%; Pred. No. 6.2; 38; Conservative 22; Mismatches 71; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.7%; Score 82.5; DB 4; Length 766; Best Local Similarity 25.4%; Pred. No. 2.3; Matches 46; Conservative 17; Mismatches 43; Indels 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application PC/TUS9400198
GENERAL INFORMATION:
APPLICANT: Schering Corp.
TITLE OF INVENTION: RAS Associated GAP Proteins
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: 5
ADDRESSE: ADDRESSE: Schering Corp.
STREET: 1 Girald Farms
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 6.0.8
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00198
                                                                                                                                                                                                                                                                                                                                                                                                      130 SDNVIKMSQLKDFNFNKPRFDFYEGA 155
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|S1 LDNIDYYLQLERNKFDSKAKDIAQKA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/004,824
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: LUMI, PAUL G.
REGISTRATION NUMBER: 32,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: DX0352 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)822-7255
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INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 766 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
      ; SEQUENCE CHARACTERISTICS:
; LENGTH: 1781 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-451-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Madison
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94304-1104
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                                                                                                                                                                  Query Match
Best Local &
                                                                                                                                                                                                       Matches
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Sequence 1752, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICATOR SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION:
FILE OF INVENTION:
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
FRIOR PILING DATE: 1999-02-13
FRIOR FILING DATE: 1998-02-13
FRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                 502 LPKTTAYHEI-WLGGDDAGDKPGYREAWENRKEGPT---KKKTLVAGN----VLADVEPQ 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 -----GMELGYALSOGKYVL---LVIPDEDYGKPIN------LMSWGVSDNVIKMSO 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                613 TYPRIGSMLGYVSKDQVHIACEKIMLVQRDFGDRTNRKHARLKYTIDDLGVDVFKAKVEE 672
                                                          58 YLHDKVWATATY-NNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDE 116
                                                                                                        ----FNFNKPRFDFYEGAV 156
562 AIBLLDELSTLRLVDKENRYEPLTSEVEKEFIDLDALYERIRAERDALQDVHRAICDHNE 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPKKTIYFGAGWF--TDRQNK-AYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Patent No. 5641666
GENERAL INFORMATION:
APPLICANT: Vahlensieck, Hans-Friedrich
APPLICANT: Hinnen, Albert
ITLE OF INVENTION: Fungi Resistant to Soraphen A
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Ciba-Geigy Corporation
STREET: Patent Dept., 520 White Plains Rd., POB 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 Y----LHDKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGL---
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JS-09-489-039A-11745
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US-09-134-001C-4707
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Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERBNCE: 032796-032

CURRENT FILING DATE: 1990-08-13

PRIOR PELICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER: OF SEQ ID NOS: 6812

SEQ ID NO 4783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1314 FTDNRNIHVYEAVSKTS------PLDKRFFTRGIIRTGHIRDDISIQEYLTSEA 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ------DKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVL-- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 FIDRONKAYKEAMEALKENPIIDLENSYVPLDNQY--KGIRVDEH-----PEYLH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
9.5%; Score 80.5; DB 1; Length 2237;
Best Local Similarity 26.5%; Pred. No. 19;
Matches 41; Conservative 17; Mismatches 50; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.3%; Score 78.5; DB 2; Length 170; 24.1%; Pred. No. 0.72; tive 29; Mismatches 54; Indels 2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/354,973
FILING DATE: 13-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary
REGISTRATION NUMBER: 40,403
REFERENCE/POCKET NUMBER: PF/5-19802/A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: 1.RNGTH: 2237 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 35; Conserv
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HYPOTHETICAL: NO
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6 IYFGAGWFT--DRONKAYKRAMBALKE-NPTIDLENSYVPLDNOYKGIRVDEHPBYLHDK 62

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Sequence 407, Application US/09134001C

Sequence 40380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-01-14

NUMBER OF SEQ ID NOS: 5674

LENGTH: 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PAPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
LENGTH: 338
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                                                                                                            66 MIALA----DTENVLASDLLVALLDGPTIDAGVASEIGVAYAKGIPVVALYTDSRQQG-- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 NDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYG-KPINLMSWGV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 QGVQPTKTQT-----VPVTDTTGMLYDLGFV------DKDLADRSGNADSFRV 114
                                                                  63 VWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPD-EDYGKP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 TDKNGRIAKIVEQLAKSNDVI-TDAIYVPCNDGSKHKTTIRAG----IPEPVW--RRYN 72
15 IYFAGPLFSQADLRYNAY--LVEQIRQLDKTIDL---YLPQEN----AAINDKSAYADSK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 TDRONKAYKEAMEALKENPTIDLENSYVPLDNOYK---GIRVDEHPBYLHDKVWATATYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.0%; Score 76.5; DB 2; Length 338; Best Local Similarity 25.2%; Pred. No. 3.4; Matches 36; Conservative 21; Mismatches 53; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
9.0%; Score 76; DB 2; Length 279;
Best Local Similarity 21.0%; Pred. No. 2.9;
Matches 39; Conservative 28; Mismatches 49; Indels
                                                                                                                                                                                                      122 INLMSWGVSDNVIKMSQLKDFNFNK 146
                                                                                                                                                                                                                                                                     120 -----ADNHQKLDALNEIAENQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11745, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEN---MGKLQGFNNKVSRYTFY 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 SDNVIKMSQLKDFNFNKPRFDFY 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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256 GTFARATAEAYRYADILAKENGKYTADLEDGGYTINIRPAGKKVDEKPEEPMD-----T 309
                                                                                                                                    104 SQGKYVLLVIPDEDYGKPINLMSW------GVS---DNVI--KMSQLKDFNFNK 146
                                                                                                                                                                                                                                  6 IYFGAG----WFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDK 62
                                            ----YDNRHYTKTINSKIEHL--S 49
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8
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APPLICANT: Bjvrck, Lars
APPLICANT: Sjvbring, Ulf
ATTLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.0%; Score 76; DB 1; Length 434; Best Local Similarity 35.8%; Pred. No. 5.5; Matches 24; Conservative 9; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: ILM PC COMPATIDLE
TILING DATE: 11-FEB-1997
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: MCMASTERS, DAVID D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.402D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                   63 VWATATYNNDLNGIKTNDIMLGVYIPDEEDVGL-
                                 Sequence 3, Application US/08795475 Patent No. 5965390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acida
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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164 SKANFY 169
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8
                                                                                APPLICANT: Bjorck, Lare
Sjobilag, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
STREET: Seed IP Law Group
STREET: 701 Fifth Avenue Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 58, Application US/08307499
Patent No. 5651972
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Myer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Glbbs, E.P.J.
TITLE OF INVENTION: Live Vaccine Vector
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISPROY disk
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,278B
FILING DATE: 26-OCt-1994
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-325-278B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: POLCET, Jane B. R.
REGISTRATION NUMBER: 33,432
REFERENCE/DOCKET NUMBER: 100084.402
TELECOMMUICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFRAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECTLE TYPE: protein
HYPOTHETICAL: NO
                Sequence 3, Application US/08325278B Patent No. 6822075 GENERAL INFORMATION:
                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                  COUNTRY: USA
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JS-08-325-278B-3
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 -----YALSQGKYVLLVIPDEDY----GKPINLMSWGVSDNVIKMSQL----KDF 142
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| Sequence 58 Application US/09299268
| Sequence 58 Application US/09299268
| Patent No. 6217845|
| Patent No. 6217845|
| Patent No. 62178410N:
| APPLICANT: Moyer, Richard W. APPLICANT: Gibbs, E.J.
| TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a TITLE OF INVENTION: Live Vaccine Vector NUMBER OF SEQUENCES:
| NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS: 61 STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.9%; Score 75.5; DB 1; Length 181;
25.8%; Pred. No. 1.7;
tive 24; Mismatches 31; Indels 3
                                                                                                 COUNTRY: U.S.A.

ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,499
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
PRIOR APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
RELEPAX: 904-375-5800
RINFORMATION POR SES: FEMALEY
FEMALEY-RETERINGER: SEQUENCE CHARACTERISTICS:
FEMALEY-RETERINGER: SEQUENCE CHARACTERISTICS:
FEMALEY-REAL PARIOR ACIDS
FEMALEY-RETERISTICS:
FEMALEY-REAL PARIOR ACIDS
: 2421 N.W. 41st Street, Suite A-1
Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 181 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 25.8
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-307-499-58
                                                                   Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFNK 146
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                                                                                              COUNTRY:
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Patent No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION:
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR PRILING DATE: 1998-02-13
PRIOR PRILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PRILING DATE: 1998-08-13
PRIOR PRILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 NDIVEFCEYIANKGKIVIVAALDGTYERRPFGNILNLIP--LSEKVTKLNAICMICHRDA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 DNQYKGIRVDEHPEYLHDKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELG--- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 -----YALSQGKYVLLVIPDEDY-----GKPINLMSWGVSDNVIKMSQL-----KDF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.9%; Score 75.5; DB 2; Length 181; 25.8%; Pred. No. 1.7;
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Mismatches
                                                                                                                                                                                                                                                                                                                                           FILING DATE:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFFICATION NUMBER: US 07/342,212
PRIOR APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFFICATION:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
FILING DATE: 31.794
REGISTRATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCC
TELECOMMUNICATION INFORMATION:
TELEBHONE: 044-375-9100
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/901,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 181 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 25.8%
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 904-172-5800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 NFNK 146
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Search completed: December 23, 2005, 22:05:47 Job time: 50 secs

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√ Wed Dec 28 10:17:20 2005

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Sequence 95, Appl
Sequence 93, Appl
Sequence 80, Appl
Sequence 86, Appl
Sequence 2176, Ap
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17, Appl
17, Appl
17, Appl
27,59, A
8723, A
8724, Ap
17, Appl
12, Appl
12, Appl
197, Appl
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8865, Ap
8866, Ap
180891,
                                                        December 23, 2005, 22:04:24; Search time 165 Seconds (without alignments) 397.571 Million cell updates/sec
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                                                                                                                     1 MPKKTIYFGAGWFTDRQNKA......QLKDFNFNKPRFDFYEGAVY 157
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USII_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-800-198-80
US-09-800-129-86
US-09-833-245-2176
US-09-808-602-17
US-09-808-602-17
US-09-808-602-17
US-09-800-198-17
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US-11-097-143-27759
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US-10-472-928-1270
US-10-282-122A-48649
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US-10-174-677-9
US-10-080-334-197
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US-10-080-334-196
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                                                                                                                                                                      1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                       sw model
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Gapop 10.0 , Gapext 0.5
                                       - protein search, using
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Maximum DB seq length: 200000000
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848
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Match Length DB
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Sequence 1998, Ap Sequence 294967, Sequence 228, App Sequence 228, App Sequence 5173, A Sequence 52533, A Sequence 1068, App Sequence 1068, App Sequence 15, Appl Sequence 1659, App Sequence 10617, A Sequence 10617, A Sequence 10617, A Sequence 10617, A Sequence 248274, Sequence 248274, Sequence 248274, Sequence 248278,	and Nuclec Acids Encoding Same	Length 464;  Indels 25; Gaps 5; GIRVDEHPEYLHDKV 63 GIRVDHPOYRQNE- 309 GLGWELGYALSQGK 107
US-10-369-493-1998 US-10-425-115-294967 US-10-840-512-228 US-10-840-51753 US-10-840-51753 US-10-732-923-821 US-10-732-923-821 US-10-732-923-9638 US-10-732-923-9638 US-10-732-923-9638 US-10-732-923-9638 US-10-732-923-9638 US-10-732-923-9638 US-10-732-923-10596 US-10-732-923-10596 US-10-732-923-10596 US-10-732-923-10596 US-10-732-923-10596 US-10-732-923-10596 US-10-732-923-10596 US-10-732-923-10596 US-10-732-923-10596 US-10-732-923-10596 US-10-732-923-10596 US-10-732-923-10596 US-10-732-923-10596 US-10-732-923-10596	NTS 1 Proteins 2	e 85.5; DB 3; No. 3.9; Ismatches 49; TIDLENSYVPLDNOYK ::: : :       SVNVFLGHTAIDEMLK MLGVYIPDEEDV :    :      VLPVCLPDNETLYRSG
2.20 2.4.4.4.4.4.6.99 2.2.99 2.2.99 2.2.99 2.2.99 2.3.33 2.33 2.33 2.33 2.33 2.33 2.33 2.33 2.33 2.33 2.33 2.33 2.33 2.33 2.33 2.	1150 51157 51157 Corin Corin 1, No 1, No 1, No 10,	0 - KK 1 - B 0-0 - F
28 30 31 31 33 33 33 33 33 34 44 40 41 44 45 46 47 48 48 48 48 48 48 48 48 48 48	RESULT 1 US-09-808-602-95 Sequence 95, Applica Patent No. US2002015 GENERAL INFORMATION: APPLICANT: Vernet, APPLICANT: Pernand APPLICANT: Majunde APPLICANT: MacBoug APPLICANTON NETRING DATE: PRIOR APPLICATION N PRIOR FILING DATE: NUMBER OF SEQ ID NO SEQ ID NO 95 LENGTH: 464 TYPE: PRT COGANISM: HOMO SAP COGANISM: HOMO SAP COGANISM: HOMO SAP	Ouery Match Guery Match Best Local 30 Y 251 Y 64 b 310 Y 108 b 368 b 368 b 368

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333 --SHNFSGDIALLELQHSIPLGPNVLPVCLPDNFTLYRSGLLGYVSGFGMEMGWLTTELK 390
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                                 274 GDRWILTAAHTVYPKDSVSLRKNQSVNVFLGHTAIDEMLKLGNHPVHRVVVHPDYRQNE- 332
                                                                                                          64 WATATYNNDL-----NGIKTNDIMLGVYIPDEEDV------GLGMELGYALSQGK 107
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9 GAGWFIDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYK-----GIRVDEHPEYLHDKV
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10.0%; Score 84.5; DB 3;
Best Local Similarity 23.1%; Pred. No. 4;
Matches 30; Conservative 26; Mismatches 49;
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JERREREMON. 13 Human secreted proteins TITLE OF INVENTION: 32 Human secreted proteins FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR PILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 86
LENGTH.: 396
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; bublication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins; FILE REFRENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR PAPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
; PRIOR PEPLICATION NUMBER: 60/256, 331
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PALENTING DATE: 2000-04-25
; SOFTWARE: PALENTING DATE: 2000-04-25
; SOFTWARE: PALENTING DATE: 2000-04-25
; SURVER FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 86, Application US/09800729
Patent No. US20020068319A1
GENERAL INFORMATION:
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US-09-800-729-86
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                                                                   APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Herrman, John L
BAPPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Masca, Peter S
ITLEOF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
FILE REPRENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT APPLICATION NUMBER: US/09/800,198
PRIOR PILING DATE: 2001-03-05
PRIOR PILING DATE: 2001-03-05
PRIOR PILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 93
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Publication No. US20030087816A1
GENERAL INFORMATION:
APPLICANT: Vernet, Cornie AM
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Masee, Peters S
APPLICANT: Masee, Peters S
APPLICANT: Rastelli, Luca
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 1596-697
CURRENT APPLICATION NUMBER: US/09/800,198
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR APPLICATION NUMBER: 60/186,596
MINNED OF OT N. NO. 0.00-03-03
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                         Vernet, Corine A
Fernandes, Elma
Shimkets, Richard A
Herrman, John L
Majunder, Kumud
Mishra, Vishnu
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Best Local Similarity 23.14
Matches 30; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 80
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; ORGANISM: Homo sapiens
US-09-808-602-93
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ORGANISM: Homo sapiens
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Matches 30; Conserva
  GENERAL INFORMATION:
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25; Gaps

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APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Herman, John L
APPLICANT: Mishra, Vishnu
APPLICANT: Mishra, Vishnu
APPLICANT: Mozes, Reter S
APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same FILE REFERENCE: 129566-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT PILING DATE: 2001-03-14
                                                                         APPLICANT: Mishra, Vishnu APPLICANT: Meses, Peter S
APPLICANT: Meses, Peter S
APPLICANT: Meses, Peter S
APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
FILE REPREBNCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
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PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
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Patent No. US20020155115A1
GENERAL INFORMATION:
Shimkets, Richard
Herrman, John L
Majumder, Kumud
Mishra, Vishnu
Mezes, Peter S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 23.1%
Matches 30; Conservative
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SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Shinkets, Richard A
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Maczes, Peters
APPLICANT: Maczes, Peters
APPLICANT: Maczes, Peters
APPLICANT: Maczes, Peters
APPLICANT: Maczes, Poters
APPLICANT: NOWBER: US/09/808,602
CURRENT APPLICATION NUMBER: US/09/800,198
PRIOR PILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARR: PaterIn Ver. 2.1
SSOFTWARR: PaterIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 GDRWILTAAHTIYPKDSVSLRKNQSVAVFLGHTAIDEMLKLGNHPVHRVVVHPDYRQNE- 297
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                                                                                                                                                                                                                          251 GDRWILTAAHTIYPKDSVSLRKNQSVAVFLGHTAIDEMLKJGNHPVHRVVVHPDVRQNB- 309
                                                                                                                                                                                                                                                                                                      64 WATATYNNDL------NGIKTNDIMLGVYIPDBEDV------GLGMELGYALSQGK 107
                                                                                                                                                                                                                                                                                                                                  9 GAGWFTDRQNKAYKEAMEALKENPT1DLENSYVPLDNQYK-----GIRVDEHPEYLHDKV 63
                                                                                                                                                                                             9 GAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYK-----GIRVDEHPEYLHDKV 63
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                                                                                    DB 3; Length 396;
                                                                                  Query Match 10.0%; Score 84.5; DB 3; Length 3: Best Local Similarity 23.1%; Pred. No. 4; Matches 30; Conservative 26; Mismatches 49; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/09808602
Patent No. US20020155115A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30; Conservative
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ORGANISM: Homo sapiens
     ; ORGANISM: Homo sapiens
US-09-833-245-2176
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Best Local Similarity
Matches 30; Conserva
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25;

Length 487;

9 GAGWFTDRONKAYKEAMEALKENPTIDLENSYVPLDNQYK----GIRVDEHPEYLHDKV 63

Best Local Similarity 23.1 Matches 30; Conservative

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274 GDRWILTAAHTIYPKDSVSLRKNQSVNVFLGHTAIDEMLKLGNHPVHRVVVHPDYRQNE- 332
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: UNCORPORTED GENES.
TITLE OF INVENTION: UNCORPORTED GENES.
THER ERFERENCE: CLOODY28
CURRENT PELLOCATION NUMBER: 105/11/097,143
CURRENT FILING DATE: 2005-04-04
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Best Local Similarity 23.1%; Pred. No. 5.4;
Matches 30; Conservative 26; Mismatches 49; Indels 2
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PRIOR FILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-19

PRIOR PILING DATE: 1999-10-19

PRIOR PILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-11-12

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-03-23

NUMBER: OF SEQ ID NOS: 43008

SEQ ID NO 27759

LENGTHH: 1537
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Publication No. US20050208558A1
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 487
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APPLICANT: Venter, J. Craig
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                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-800-198-19
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                                                                                                                          333 --SHNFSGDIALLELQHSIPLGPNVLPVCLPDNETLYRSGLLGYVSGPGMEMGMLTTELK 390
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   274 GDRWILTAAHTIYPKDSVSLRKNQSVNVFLGHTAIDEMLKLGNHPVHRVVVHPDYRQNE- 332
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                                                                                           64 WATATYNNDL-----NGIKTNDIMLGVYIPDEEDV------GLGMELGYALSQGK 107
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
APPLICANT: Vernet, Cornie AM
; APPLICANT: Perrandes, Elma
; APPLICANT: Brimkets, Richard A
APPLICANT: Majumder, Kunnd
; APPLICANT: Majumder, Kunnd
; APPLICANT: Majumder, Kunnd
; APPLICANT: Maste, Perer S
; APPLICANT: Maste, Vishna
; APPLICANT: Maste, Perer S
; APPLICANT: Rastelli, Luca
; TILLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; TILLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; CURRENT APPLICATION NUMBER: US/09/800,198
; CURRENT FILING DATE: 2001-03-05
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
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| Publication No. US20030087816A1
| GENERAL INFORMATION:
| APPLICANT: Vernet, Cornie AM
| APPLICANT: Fernandes, Elma
| APPLICANT: Rinkets, Kichard A
| APPLICANT: Majumder, Kichard A
| APPLICANT: Majumder, Kumud
| APPLICANT: Majumder, Kumud
| APPLICANT: Mashra, Vishna
| APPLICANT: Rastelll, Luca
| APPLICANT: Rastelll, Luca
| TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
| FILE REFRENCE: 15966-697
| CURRENT APPLICATION NUMBER: US/09/800,198
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Matches 30, Conserv
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US-09-800-198-19
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30; Mismatches
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Publication No. US20050208558A1
GENERAL INFORMATION:
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Best Local Similarity 20.4*
Matches 42; Conservative
   42; Conservative
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ORGANISM: DROSOPHILA
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| | ::: | ::: | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : | : : : | : | : : : | : | : : : | : | : : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : | : : : | : : : | : : : | : : : | : : | : : : | : : | : : : | : | : : : | : | : : : | : | : : : | : | : : : | : | : : : | : | : : : | : | : : : | : | : : : | : | : : : | : | : : : | : | : : : | : | : : : | : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : 
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                                                                                                    80 DIMLG-----VYIPDEEDVGLGMELGYALSQGKYVLLV----IPD----EDYGKP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- DLENSYVPLDN 45
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Fublication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796) C
CURRENT PILLICATION NUMBER: US/10/132,923
CURRENT FILING DATE: 2003-12-10
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 8724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR PEDLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.9%; Score 84; DB 5; Length 1634; Best Local Similarity 20.4%; Pred. No. 32; Matches 42; Conservative 30; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 GAGWFTDRQ----NKAYKEAMEALKENPTI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 INLMSWGVSDNVIKM--SQLKDFNFN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 INLMSWGVSDNVIKM--SQLKDFNFN 145
                                                                                                                                                                                                                                                                                           :::|: | ::|
747 VGVVSYKGSPQGRRLLQNQMRATKFN 772
                                                                                                                                                   ; Sequence 8723, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 QYKGIRVDEHPEY----LHDKV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-732-923-8723
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-10-732-923-8723
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LENGTH: 1634
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APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT PILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/15/,832
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR PLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOOTHWARE: FERSEEQ for Windows Version 4.0
11
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                                                                                                                                                                                                                                                         80 DIMLG-----VYIPDEEDVGLGMELGYALSQGKYVLLV----IPD-----EDYGKP 121
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                                                                                        685 GWDWIDDEEDSCGSNDDHKPKVE---EQPTATEDATDKAQATGNDEDAKDLITKAKVEDD.
                                                                                                                                                   Gaps
86; Gaps
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48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 GAGWFTDRQ----NKAYKEAMEALKENPTI--
                                                  9 GAGWFTDRQ-----NKAYKEAMEALKENPTI--
                                                                                                                                                                                                                                                                                                                                                              122 INLMSWGVSDNVIKM--SQLKDFNFN 145
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RESULT 15
US-10-160-758-11
Sequence 11, Application US/10160758
Publication No. US20030036076A1
Sequence 11, Application No. US20030036076A1
SEDERAL INFORMATION:
TILE REFERENCE: EXO2-089C
CURRENT APPLICATION UNMBER: US/10/160,758
CURRENT FILING DATE: 2002-06-03
PRIOR PILING DATE: 2001-06-05
PRIOR PLICATION NUMBER: US 60/296,076
PRIOR PLICATION NUMBER: US 60/296,076
PRIOR PLICATION NUMBER: US 60/328,605
PRIOR PLICATION NUMBER: US 60/328,605
PRIOR PLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Version 3.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 KVWATATYNND--LNGIKTNDIMLGVYIPD---EEDVGL---GMELGYALSOGKYVLLVI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 DRQNKAYKEAMEALKE--NPTIDL-----ENSYVPLDNQ-YKGIRVDEHPEYLHD 61
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9.8%; Score 83; DB 4; Length 3354;
Best Local Similarity 22.2%; Pred. No. 1.1e+02;
Matches 36; Conservative 32; Mismatches 68; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 PDEDYGKPINLMSWGVSDNVIKMSQLKDFNFNKPRFD-FYEG 154
TYPE: PRT
CRGANISM: Homo sapiens
US-10-160-758-11
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Search completed: December 23, 2005, 22:20:26 Job time : 167 secs

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December 23, 2005, 22:05:00 ; Search time 12 Seconds (without alignments) 93.321 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA_New:*

1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/PCSO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                       54001 seqs, 7132810 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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848
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8:
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

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	g	4, Appli	1948, Ap	202, App	3, Appli	12, Appl	2, Appli	9, Appli	668, App	145, App	4, Appli	1662, Ap	1, Appli	1007, Ap	6, Appli	21, Appl	2, Appli	1, Appli	14, Appl	4, Appli	71, Appl	4, Appli	8, Appli	10, Appl	65, Appl	144, App
	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence
SUMMAKIES	OI .	US-11-070-627-4	US-10-793-626-1948	US-11-074-176-202	US-11-070-627-3	US-10-979-821-12	US-11-070-627-2	US-11-070-627-9	US-10-793-626-668	US-10-485-517-145	US-11-094-586-4	US-10-821-234-1662	US-11-070-627-1	US-10-821-234-1007	US-11-004-057-6	US-11-004-057-21	US-10-630-203-2	US-11-103-037-1	US-10-392-234A-14	US-10-467-962B-4	US-10-858-730-71	US-11-091-643-4	US-11-070-627-8	US-11-070-627-10	US-11-017-550-65	US-10-873-528-144
	图	7	9	7	7	9	7	7	9	9	7	9	7	9	7	7	9	7	9	9	9	7	,	7	7	ø
•	Match Length	750	252	756	750	391	750	786	395	1107	605	747	750	751	1302	1493	485	485	1048	959	1170	1316	770	770	932	385
* Query	Match	9.5	8.7	8.6	8.3	8.2	8.5	8.2	8.1	8.1	8.0	8.0	8.0	8.0	8.0	8.0	7.9	7.9	7.9	7.8	7.8	7.8	7.8	7.8	7.8	7.7
	Score	78	73.5	73	70.5	69.5	69.5	69.5	68.5	68.5	68	68	68	68	67.5	67.5	67	67	67	66.5	66.5	66.5	99	99	99	65.5
Result	No.	1	7	٣	4	ß	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Seguence 8376, Ap	Sequence 1536, Ap	Sequence 20, Appl	Seguence 5510, Ap	Seguence 2612, Ap	Seguence 604, App	ч,	Sequence 26, Appl	Seguence 22, Appl	Sequence 1004, Ap	Seguence 20, Appl	Sequence 256, App	Sequence 2, Appli	Sequence 1532, Ap	Sequence 18, Appl	Sequence 4, Appli	Seguence 358, App	Sequence 101, App	Sequence 3, Appli	Sequence 2368, Ap
US-10-467-657-8376	US-10-821-234-1536	US-10-661-966-20	US-10-467-657-5510	US-10-793-626-2612	US-10-793-626-604	US-11-094-586-24	US-11-094-586-26	US-11-188-743-22	US-10-793-626-1004	US-10-392-234A-20	US-11-074-176-256	US-11-004-057-2	US-10-821-234-1532	US-10-392-234A-18	US-11-004-057-4	US-10-485-517-358	US-11-129-143-101	US-10-617-034A-3	US-10-467-657-2368
9	9	9	9	9	9				9	9	7	7			7	9	7	9	9
728	417	739	1259	174	522	531	531	1360	338	1048	1213	672	705	1048	1493	306	306	325	459
7.7	7.7	7.7	7.7	7.6	7.6	7.6	7.6	7.6	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.4	7.4	7.4	7.4
65.5	65	65	65	64.5	64.5	64.5	64.5	64.5	64	64	64	63.5	63.5	63.5	63.5	63	63	63	63
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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273 MNKVMELEKEIANATTKSEDRNDPMLLYNKMTLAQIQNNFSLEINGKPFSWSNFTNEIMS 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 -LGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPI------NLMSWG-VS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333 TVNINIPNEEDV-----VYYA---PEYLIKL-----KPILTKYFPRDFQNLFSWRFIM 377
Sequence 4, Application US/11070627

Sequence 4, Application US/11070627

Publication No. US20050271625A1

GENERAL INFORMATION:

APPLICANT: Burger, Corinna

TITLE OF INVENTION: RAAV-NEPRILYSIN COMPOSITIONS AND METHODS OF USE

FILE REFERENCE: 36689.

CURRENT APPLICATION NUMBER: US/11/070,627

CURRENT APPLICATION NUMBER: 60/549,399

PRIOR APPLICATION NUMBER: 60/549,399

PRIOR APPLIANG DATE: 2006-03-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin version 3.3

SEQ ID NO 4

LENGTH: 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----PEYLHDKVWATATYNN---DLNGIK-----TNDIM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MPKKTIYFGAGWPTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            78;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
9.2%; Score 78; DB 7; Length 750;
Best Local Similarity 23.4%; Pred. No. 3.4;
Matches 44; Conservative 25; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Oryctolagus cuniculus US-11-070-627-4
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DLVSSLSR 385
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                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Sequence 1948, Application US/10793626; Publication No. US20050255478A1 GENERAL INCRWATION: APPLICANT: KIMMERLY, WILLIAM JOHN

us-10-049-750-14.rapbn

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 LHDKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVG-----LGMELGYALSQGKYVLLVI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 TDAGKIFFKKCQEIIALYDNLPTEINSLYGLETGHITISMSAVMSMRKFIGVLGDFH--- 72
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 TDRQNKAYKEAME--ALKEN-PT----IDLENSYVPLD-----NQYKGIRVDEHPEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20.4. Application US/110/4176
Sequence 20.4. Application No. USCO050250135A1
GENERAL INFORMATION:
APPLICANT: Rusell, William M.
APPLICANT: Rusell, Milliam M.
APPLICANT: Rusell, Milliam M.
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR FILING DATE: 2006-03-08
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               54; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                               8.7%; Score 73.5; DB 6; Length 252; 24.5%; Pred. No. 2.2; tive 29; Mismatches 54; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 8.6%; Score 73; DB 7; Length 756; 1 Similarity 24.7%; Pred. No. 11; 23; Conservative 19; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 PDEDYGKPINLMSWGVSDNVIKMSQLKDFNFNKPRFDFY 152
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                   FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1948
LENGTH: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT : ORGANISM: Lactobacillus acidophilus US-11-074-176-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 202, Application US/11074176
; Publication No. US20050250135A1
                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             39; Conservative
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Best Local Similarity
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Best Local Similarity
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LENGTH: 756
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 A---LSQGKYVLLVIPDEDYGKPINLMSWG-VSDNVIKMSQLKDFNFNKPRFDFYEGAVY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 APEYLTKIKPILIKYSPRDLQ---NLMSWRFIMDLVSSLSR----NYKESR-NAFRKALY 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 ---PEYLHDKVWATATYNN---DLNGIK-----TNDIM--LGVYIPDEEDVGLGMELGY 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 RNDPMLLYNKMTLAKLONNFSLEVNGKSFSWSNFTNEIMSTVNINIONEEEV-----VVY 347
Sequence 3, Application US/11070627

Publication No. US20050271625A1

FORDERAL INFORMATION:
TOTAL OF INVENTION: AAV-NEPRILYSIN COMPOSITIONS AND METHODS OF USE
TITLE OF INVENTION: LAAV-NEPRILYSIN COMPOSITIONS OF USE
FILE REFERENCE: 36689.8

CURRENT APPLICATION NUMBER: US/11/070,627

FILE REFERENCE: 2005-03-02

PRIOR APPLICATION NUMBER: 60/549,399

PRIOR PILING DATE: 2004-03-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin version 3.3

LENGTH: 750
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APPLICANT: ARRAHAM, TIMOTHY W.
APPLICANT: HICKS, PAULA M.
APPLICANT: HICKS, PAULA M.
APPLICANT: MILLIS, JIM
APPLICANT: ROSAZZA, JACK
APPLICANT: ZHAO, LISHAN
APPLICANT: ZHAO, LISHAN
APPLICANT: WEINER, DAVID P.
TITLE OF INVENTION: PRODUCTION OF MONATIN AND ITS PRECURSORS
FILE REPERENCE: 023829-0390
CURRENT APPLICATION NUMBER: US/10/979,821
CURRENT FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature; LCCATION: (38)...(38); OTHER INFORMATION: Xaa can be any naturally occurring amino acid 105-11-070-627-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 69.5; DB 6; Length 391;
Pred. No. 9.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
8.3%; Score 70.5; DE
Best Local Similarity 24.4%; Pred. No. 18;
Matches 44; Conservative 27; Mismatches
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PRIOR APPLICATION NUMBER: 10/422,366
PRIOR FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: 60/374,831
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIN Ver. 3.3
SEQ ID NO 12
LENGTH: 391
TYPE: RRT
TYPE: RRT
CREANISM: Lactobacillus amylovorus
US-10-979-821-12
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Publication No. US20050244937A1
GENERAL INFORMATION:
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Best Local Similarity
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                                                         273 MNKVMELEKEIANATTKPEDRNDPMLLYNKMTLAKLQNNFSLEINGKPFSWSNFTNEIMS 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 -LGVYIPDEEDVGLGMELGYA---LSQGKYVLLVIPDEDYGKPINLMSWG-VSDNVIKMS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 TVNINIQNEEEV-----VVYAAPEYLTKIKPILTKYSPRDLQ---NLMSWRFIMDLVSSLS 384
                                                                                                          71 NDLNGIKTNDIM-----LGVYIP--DEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPIN 123
                                                                                                                                 216 ----GVKHFSIASLIPERAIYISGLSKSHAMTGYRLGYVAGPAKIM-----AEIGKVHG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 -----DLNGIK-----TNDIM- 82
                                22 KEAMEALKENPTID----LENSYVPLDNQYKGIRV------DEHPEYLHDKVWATATYN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/11070627

Publication No. US20050271625A1

GENERAL INFORMATION:

APPLICANT: Nagh, Kevin R.

APPLICANT: Burger, Corinna

TITLE OF INVENTION: rAAV-NEPRILYSIN COMPOSITIONS AND METHODS OF USE

FILE REPRESENCE: 36689.8

CURRENT PAPLICATION NUMBER: US/11/070,627

CURRENT FILING DATE: 2005-03-02

PRIOR PILING DATE: 2004-03-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin version 3.3

SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MPKKTIYFGAGWFIDRONKAYKEAMEALKENPIIDLENSYVPLDNQYKGIRVDEH----
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 Gaps
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                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/11070627
Publication No. US20050271625A1
GENERAL INFORMATION:
APPLICANT: Nash, Kevin R.
APPLICANT: Burger, Corinna
TITLE OF INVENTION: RAAV-NEPRILYSIN COMPOSITIONS AND METHODS OF 19; FILE REPERENCE: 36689.8
CURRENT APPLICATION NUMBER: US/11/070,627
FILE REPERENCE: 2005-03-02
PRIOR EPLING DATE: 2004-03-02
PRIOR FILING DATE: 2004-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.2%; Score 69.5; DB 7; Length 750; Best Local Similarity 23.5%; Pred. No. 23; Matches 47; Conservative 29; Mismatches 55; Indels 6
 52; Indels
 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 QLKDFNFNKPRFDFYEGAVY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Rattus norvegicus
US-11-070-627-2
32; Conservative
                                                                                                                                                                                  124 LMSWGVSDN 132
                                                                                                                                                                                                                     266 LMVTTTTDS 274
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64 WATATYNN---DLNGIK-----TNDIM--LGVYIPDEEDVGLGMELGYA---LSQGKYV 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 OGYNSWCAGYTMSALFNATYNTNRYNAESVMRYLHPNLRGHDFQFTGLTSNEMLRFGRSQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 -------NDLNGIKTND---IMLGVYIPDEEDVGLGMELGYA----LSQGKYVL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 GRNTQYLNRMTSYNEVDQLTTNNQGIAVLGKRVESSDGIHAGHAMAVAGNAKVNNGQKVI 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 668, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                              14 TDRQN-KAYKEAMEALK-----ENPTIDLENS----YVPLDNQYKGIRVDEH
                                                                                                                                                                                                                  9 GAGWFTDRQNKAYKEAMEALKENPTIDLENSYV----PLDNQYKGIRVDEHPEYLHDKV
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic;
; OTHER INFORMATION: amino acid sequence
0S-10-793-626-668
                                                                                                                                                                   41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 LLVIPDEDYGKPINLMSWG-VSDNVIKMSQLKDFNFNKPRFDFYEGAVY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:| | | : | : | : | : | : | TIWIPWDNG----LMTODAHSNIIPVS-----NGDHYEWY-ASIY 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 LVIPDEDYGKPINLMSWGVSDNVIKMSQLKDFNFNKPRFDFYEGAVY 157
                                                                                                                                                                   58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                     DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18:1%; Pred. No. __.
rive 33; Mismatches
                                                                                                                                                                   28; Mismatches
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8.1%; Pred. No. 12;
                                                                                                                   Score 69.5; 1
Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                   Query Match
Best Local Similarity 24.9%;
Matches 42; Conservative 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Conservative
                    TYPE: PRT
ORGANISM: Canis familiaris
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Matches 41; Conserval
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                                                                     US-11-070-627-9
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LENGTH: 786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 PEYLHDKVWATATYNNDL--NGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVI 113
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618 QAQALNEAMKALKESIKDQPQTBASSKFINEDQAQKDAYTQAVQHAKDLINKTTDPTLAK 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 ------RVDEHPRYLH------DKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGL 95
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                                                                                                                                                                                                                                                                                                                                                                                                                     65; Indels
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APPLICANT: Butler, Karlene H.
APPLICANT: Butler, Karlene H.
APPLICANT: Carlson, Thomas J.
APPLICANT: Garlson, Thomas J.
APPLICANT: Garlson, Thomas J.
APPLICANT: Stop, Johan M.
TITLE OF INVENTION: Plastidic Phosphoglucomutase Genes FITLE REFERENCE: BH151 USCIP
FILLE REFERENCE: BH21 USCIP
CURRENT APPLICATION NUMBER: US 09/906,209
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 32
SOFTWARRE: Microsoft Office 97 & Patentin Version 3.3
SEQ ID NO 4
LUNGTH: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 QNKAYKEAMEALKEN----PTIDLENSYVPLDNQYKGI-----
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1 Similarity 29.5%; Pred. No. 24;
31; Conservative 17; Mismatches
APPLICANT: Foster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REPERRNCE: P100629W0
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR PILING DATE: 2001-08-02
PRIOR PLING DATE: 2002-01-09
PRIOR PILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: Patentin version 3.1
SEQ ID NO 1455
                                                                                                                                                                                                                                                                                                                                                                            8.1%; Score 68.5; D
20.4%; Pred. No. 48;
tive 26; Mismatches
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                                                                                                                                                                                                                                                                                                               ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 20.4 Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Zea mays
US-11-094-586-4
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Best Local S:
Matches 31
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Andamani, Susan
APPLICANT: Andamani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR PAPLICATION NUMBER: US 60/462,047
PRIOR PAPLICATION OF 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SEQ ID NO 1662
LENGTH: 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MPKKTIYFGAGWFTDRQNKAYKBAMEALKENPTIDLENSYVPLDNQYKGIRVDEH----
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Fublication No. US20050271625A1
GENERAL INFORMATION:
APPLICANT: Nash, Korin R.
APPLICANT: Burger, Corinna
TITLE OF INVENTION: rAAV-NEPRILYSIN COMPOSITIONS AND METHODS OF USE
FILLE REPRESENCE: 36689.8
CURRENT APPLICATION NUMBER: US/11/070,627
CURRENT FILING DATE: 2005-03-02
PRIOR APPLICATION NUMBER: 60/549,399
FRIOR RELIGATION NUMBER: 60/549,399
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTING DATE: 2004-03-02
NUMBER OF SEQ ID NOS: 11
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114 -PDEDYGKPINLMSWGVSDNVIKMSQLKDFNFNKPRFDFYEGAVY 157
                            230 DPVSDY---LELM----ENVFDFQLIKDL-LSRPDFRFIFDAMH 265
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Pred. No. 32;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.0%; Score 68; DB 24.3%; Pred. No. 32; tive 23; Mismatches
                                                                                                                                                                     Sequence 1662, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
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Best Local Similarity 38.2%;
Matches 13; Conservative
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Best Local Similarity 24.3*
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-821-234-1662
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US-11-004-057-21
Matches
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Sequence 6, Application US/11004057

PUBLICALION NO. US20050244846A1

GENERAL INFORMATION:

APPLICANT: Johnson, Gary L.

TITLE OF INVENTION: MRKI PROTEINS AND FRAGMENTS THEREOF FOR USE IN REGULATING TITLE OF INVENTION: MRKI PROPENSIS

CURRENT PELLICATION NUMBER: US/11/004,057

CURRENT FILING DATE: 2000-05-10

PRIOR FILING DATE: 2000-05-10

NUMBER OF SEQ ID NOS: 21

SOFTWARR: PATCHLING VET: 2.0

SOFTWARR: PATCHLING VET: 2.0
                                                                                                                              Sequence 1007, Application US/10821234

; Sequence 1007, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Van
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Andarmani, Susan
; TILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2003-04-07
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 LPSRDYYECTG-----IYKEACTAY-----VDFMISVARLIRQEERLPIDENQLALE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 MNKVMELEKEIANATAKPEDRNDPMLLYNKWRLAQIQNNFSLEINGKPFSWLNFTNEIMS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 -LGVYIPDEEDVGLGMELGYA---LSQGKYVLLVIPDEDYGKPINLMSWG-VSDNVIKMS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
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Pred. No. 74;
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Best Local Similarity 24.3%; Pred. No. 32;
Matches 44; Conservative 23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1007
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ORGANISM: Homo sapiens
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Best Local Similarity
                                              385 R 385
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                   138 Q 138
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Sequence 21, Application US/11004057

Publication No. US20050244846A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MEKKI PROTEINS AND FRAGMENTS THEREOF FOR USE IN REGULATING TITLE OF INVENTION: APOPTOSIS
FILE REFERENCE: CPI-042CPPC
CURRENT PAPLICATION NUMBER: US/11/004,057
CURRENT FILING DATE: 2004-12-02
PRIOR APPLICATION NUMBER: US/09/403,075
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 21
SOFFWARE: Patentin Ver: 2.0
SEQ ID NO 21
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                                                                                1155 NOKCKEKMEAEBEBEALAIAMAMSASQDALPIVPQLQVENG-----EDIIIIQADT-PETL 1208
9
                                                                                                                                                                                            1018 PGHTKAKQPYREDAEWLKGQQİGLGAFSSCYQAQDVGTĞTLM-.AVKQVTYVRNTSSEQE 1075
                                                                                                                                              60 HDKVWATATYNNDLNGIKTNDIMLGVYIP--DEEDVGLGMELGYALSQGKYVLLVIPDED 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 HDKVWATATYNNDLNGIKTNDIMLGVYIP--DEEDVGLGMELGYALSQGKYVLLVIPDED 117
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                                                 ----PTIDLENSYVPLDNQYKGIRVDEHPEYL 59
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  35; Gaps
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  62;
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;; Pred. No. 89;
20; Mismatches
  21; Mismatches
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                                                   18 NKAYKEAMEALKEN-----
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Best Local Similarity 24.5%;
Matches 38; Conservative 2
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     37; Conservative
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Sequence 14, Application US/10049750
GENERAL INFORMATION:
APPLICANT: Tischer, Wilhelm
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                                                                                                                  December 23, 2005, 21:57:09 ; Search time 569 Seconds (without alignments) 381.313 Million cell updates/sec
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1 MPKKTIYFGAGWFTDRQNKA......QLKDFNFNKPRFDFYEGAVY 157
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Sequence 2174, Ap
Sequence 2174, Ap
Sequence 6487, Ap
Sequence 10210, A
Sequence 96101, A
Sequence 18384, A
Sequence 18384, A
Sequence 22, Appl
Sequence 48, Appl
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8, Appli
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Sequence 1449, Ap
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Sequence 4
Sequence 4
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US-11-097-292-2

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US-11-097-292-14

US-10-07-292-14

US-10-07-292-14

US-10-07-292-16

US-11-097-292-16

US-10-07-292-16

US-10-097-292-16

US-10-097-292-16

US-10-097-292-16

US-10-097-292-16

US-10-097-292-16

US-10-097-292-17

US-09-791-537-96101

US-09-791-79-79-98

US-09-801-79-79-98

US-09-803-245-772-38

US-09-803-245-2176

US-09-8
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| GENERAL INFORMATION:
| APPLICANT: KAMINSKI, PIERRE-ALEXANDRE
| APPLICANT: TAILLIEZ, PATRICK
| APPLICANT: TAILLIEZ, PATRICK
| APPLICANT: OURNER: PASCAL
| APPLICANT: COTAYA, RACHEL
| APPLICANT: COTAYA, RACHEL
| TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES, CORRESPONDING
| TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES, CORRESPONDING
| TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES, CORRESPONDING
| TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES, CORRESPONDING
| TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND THEIR USES
| FILE REFERENCE: 2502460SORPOT
| CURRENT FILING DATE: 2001-09-14
| PRIOR FILING DATE: 2001-09-14
| PRIOR FILING DATE: 2001-09-14
| PRIOR FILING DATE: 2002-09-12
| NUMBER OF SEQ ID NOS: 16
| SEQ ID NOS: 16
| SEQ ID NO 2.
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               APPLICANT: Barzu, Occavian
APPLICANT: Sakamoto, Hiroshi
APPLICANT: Sakamoto, Hiroshi
APPLICANT: Pistornik, Elisabeth
APPLICANT: Pochet, Sylvie
TITLE OF INVENTION: Enzymatic synthesis of deoxyribonucleosides
TITLE OF INVENTION: Enzymatic synthesis of deoxyribonucleosides
TITLE OF INVENTION: Enzymatic synthesis of deoxyribonucleosides
CURRENT FILING DATE: 2002-02-15
FRIOR APPLICATION NUMBER: EP99116425.2
PRIOR APPLICATION NUMBER: EP99116425.2
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENTH: 157
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82.6%; Pred. No. 2.8e-73;
iive 20; Mismatches 7;
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ORGANISM: Lactobacillus leichmannii
Ihlenfeldt, Hans-Georg
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Best Local Similarity
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Matches 128
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APPLICANT: TAILLIEZ, PRIERRE-ALEXANDRE
APPLICANT: TAILLIEZ, PHILIPPE
APPLICANT: TAILLIEZ, PHILIPPE
APPLICANT: QUENEE, PASCAL
APPLICANT: COTANA, RACHEL
TITLE OF INVENTION: LACTORACILLUS N-DEOXYRIBOSYL TRANSFERASES, CORRESPONDING
TITLE OF INVENTION: LACTORACILLUS N-DEOXYRIBOSYL TRANSFERASES,
TITLE OF INVENTION: LACTORACILLUS N-DEOXYRIBOSYL TRANSFERASES,
CURRENT APPLICATION NUMBER: US,11/097,292
CURRENT PILING DATE: 2005-04-04
PRIOR PILING DATE: 2005-04-04
PRIOR PILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATCHIN VERSION 3.3
SEQ ID NO 14
LENGTH: 158
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APPLICANT: TAILLIEZ, PATRICK
APPLICANT: TAILLIEZ, PATRICK
APPLICANT: MARLIERE, PHILIPPE
APPLICANT: OCTAYA, RACHEL
TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES, CORRESPONDING
TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES,
TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES,
TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES,
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TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES,
CURRENT FILING DATE: 2005-04-04
FRIOR RELING DATE: 2005-04-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 NLMSWGVCDNAIKISELKDFDFNKPRYNFYDGAVY 158
                                                                                                                                               124 NIMSWGVCDNAIKISELKDFDFNKPRYNFYDGAVY 158
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                                                                                               123 NLMSWGVSDNVIKMSQLKDFNFNKPRFDFYEGAVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KAMINSKI, PIERRE-ALEXANDRE APPLICANT: TAILLIEZ, PATRICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/11097292 GENERAL INFORMATION:
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RESULT 8
US-09-791-537-8009
US-60-711-491-264
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Klaenhammer, Todd
APPLICANT: Rlaenhammer, Todd
APPLICANT: Rateseall, William
APPLICANT: Altermann, Eric
TITLE OF INVENTION: LACTOBACILLUS ACIDOPHILUS NUCLEIC ACIDS AND USES THEREOF
FILE REFERENCE: 035051/296336
CURRENT FILING DATE: 2005-26
NUMBER OF SEQ ID NOS: 2561
SOFTWARE: Patentin version 3.2
SEQ ID NO 264
LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-60-622-712-264

US-60-622-712-264

Sequence 264, Application US/60622712

GENERAL INFORMATION:

APPLICANT: Klaenhammer, Todd

APPLICANT: Russell, William

APPLICANT: Alterman, Eric

TITLE OF INVENTION: LACTOBACILLUS ACIDOPHILUS NUCLEIC ACIDS AND USES THEREOF

TITLE OF INVENTION LACTOBACILLUS ACIDOPHILUS NUCLEIC ACIDS AND USES THEREOF

CURRENT APPLICATION NUMBER: US/60/622,712

CURRENT APPLICATION NUMBER: US/60/622,712

CURRENT FILING DATE: 2004-10-27

NUMBER OF SEQ ID NOS: 2559

SOFTWARE: PatentIn version 3.2

SEQ ID NO 264

LENGTH: 159
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                                                                                                                                                                                                                                                            66 WASATYHNDLIGIKSSDIMLGVYLPEEEDVGLGMELGYALSQGKYILLVIPDEDYGKPIN 125
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                                                                                                                                                  4 KTIYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDKV
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84.8%; Score 719; DB 50; Length 159;
Best Local Similarity 83.1%; Pred. No. 2.9e-72;
Matches 128; Conservative 18; Mismatches 8; Indels
                                                         Query Match 84.8%; Score 719; DB 40; Length 159; Best Local Similarity 83.1%; Pred. No. 2.9e-72; Matches 128; Conservative 18; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                      126 LMSWGVCDNAIKISELKDFDFNKPRFNFYDGAVY 159
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ORGANISM: Lactobacillus acidophillus NTD
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      ; ORGANISM: Lac
US-11-097-292-12
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Sequence 8009, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
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APPLICANT: TAILLIEZ, PATRICK
APPLICANT: TAILLIEZ, PATRICK
APPLICANT: MARLIERE, PHILIPPE
APPLICANT: MARLIERE, PHILIPPE
APPLICANT: OCTAYA, RACHEL
TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES, CORRESPONDING
TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES,
TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES,
CURRENT APPLICATION NUMBER: US/11/097,292
CURRENT APPLICATION NUMBER: US/11/097,292
CURRENT APPLICATION NUMBER: PR 0 111 911
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PALCHLIN VEXBION 3.3
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84.8%; Score 719; DB 51; Length 159; 83.1%; Pred. No. 2.9e-72; ive 18; Mismatches 8; Indels
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84.2%; Pred. No. 3.5e-62;
tive 17; Mismatches 4;
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121 NRPRFNFYDGAVY 133
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                                                         Best Local Similarity 83.1
Matches 128; Conservative
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GENERAL INFORMATION:

APPLICANT: RANILEE, PATRICK

APPLICANT: MARLIERE, PHILIPPE

APPLICANT: MARLIERE, PHILIPPE

APPLICANT: OF INVENTION: UCLEOTIDE SEQUENCES

TITLE OF INVENTION: UCLEOTIDE SEQUENCES AND THEIR USES

TITLE OF INVENTION: UCLEOTIDE SEQUENCES AND THEIR USES

TITLE OF INVENTION: UCLEOTIDE SEQUENCES AND THEIR USES

TITLE OF INVENTION: UNMER: US/11/097,292

CURRENT APPLICATION NUMBER: VS/11/097,292

CURRENT PALLOR DATE: 2001-09-14

PRIOR PELLING DATE: 2001-09-14

PRIOR PELLING DATE: 2001-09-14

PRIOR PELLING DATE: 2002-09-12

NUMBER OF SEQ ID NOS: 16

SOSTWARE: PATENTIN VEFEION 3:3
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73.1%; Score 620; DB 27; Length 165;
Best Local Similarity 71.9%; Pred. No. 4.9e-61;
Matches 110; Conservative 23; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 405; DB 40; Length 84;
Pred. No. 4.1e-37;
8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                123 NLMSWGVSDNVIKMSQLKDFNFNKPRFDFYEGA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 OGKYVLLVIPDEDYGKPINLMSWG 128
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; ORGANISM: Lactobacillus helveticus
US-09-791-537-8009
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; ORGANISM: Lactobacillus crispatus
US-11-097-292-8
CURRENT FILING DATE: 2001-02-22 NUMBER OF SEQ ID NOS: 153055 SOFTWARE: Patentin version 3.0 SEQ ID NO 8009 LENGTH: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 86.9%;
Matches 73; Conservative
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US-11-097-292-6
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Sequence 6, Application US/11097292; GENERAL INFORMATION:
APPLICANT: KAMINSKI, PIERRE-ALEXANDRE
APPLICANT: TAILLIEZ, PATRICK
APPLICANT: MARLIERE, PHILIPPE
APPLICANT: QUENEE, PASCAL

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APPLICANT: TAILLIEZ, PATRICK
APPLICANT: MARITERE, PHILIPPE
APPLICANT: QUENE, PASCAL
APPLICANT: QUENE, PASCAL
APPLICANT: QUENE, PASCAL
APPLICANT: QUENE, PASCAL
TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES, CORRESPONDING
TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES,
TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES,
TITLE OF INVENTION: LACTOBACILLUS N-DEOXYRIBOSYL TRANSFERASES,
TITLE OF INVENTION: LACTOBACH SEQUENCES AND THEIR USES
FILE REPERENCE: 2502-64050 DES-04-04
CURRENT FILING DATE: 2005-04-04
FRIOR FILING DATE: 2001-09-14
FRIOR FILING DATE: 2001-09-14
FRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN Version 3.3
SOFTWARE: PATENTIN VERSION 3.3
APPLICANT: COTAYA, RACHEL
TITLE OF INVENTION: LACTOBACILLUS N-DECXYRIBOSYL TRANSFERASES, CORRESPONDING
TITLE OF INVENTION: LACTOBACILLUS N-DECXYRIBOSYL TRANSFERASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND THEIR USES
FILE REPERENCE: 2502-46USOXPCT
CURRENT FILING DATE: 2005-04-04
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2002-09-12
PRIOR PILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Lactobacillus helveticus PTD
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, APPLICANT: KAMINSKI, PIERRE-ALEXANDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Matches 49; Conserve
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Best Local Similarity
Matches 55; Conserv
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Sequence 6487, Application US/10417884
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILLE OF INVENTION: NUCLEIC FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 TATYNNDLNGIKTNDIMLGVYIPDEE--DVGLGMELGYALSQGKYVLLVIPDEDYGKPIN 123
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                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
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APPLICATION UNDRER: US/10/417,884
FILING DATE: 17-Apr-2003
PRIOR APPLICATION DATA:
APPLICATION UNTRER: US/09/107,532A
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
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| | :::::| | : | |
| LMITQSLHTYLKSDQAVREYDFETLPVETYVG 153
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Query Match
10.8%; Score 91.5; Di
Best Local Similarity 23.0%; Pred. No. 0.28
Matches 35; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...156
SEQUENCE DESCRIPTION: SEQ ID NO: 6487:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8077
INFORMATION FOR SEQ ID NO: 6487:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                           CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                              g
                                                                                                                                                                 Sequence 2174 Application US/60622712
GENERAL INFORMATION:
APPLICANT: Klaenhammer, Todd
APPLICANT: Russell, William
APPLICANT: Alterman, Eric
TITLE OF INVENTION: LACTOBACILLUS ACIDOPHILUS NUCLEIC ACIDS AND USES THEREOF
FILE REFERENCE: 5051-604FND NUMBER: US/60/622,712
CURRENT APPLICATION NUMBER: US/60/622,712
NUMBER OF SEQ ID NOS: 2559
SOFTWARE: Patentin version 3.2
SEQ ID NO 2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Klaenhammer, Todd
APPLICANT: Russell, William
APPLICANT: Russell, William
APPLICANT: Russell, William
APPLICANT: Altermann, Eric
TITLE OF INVENTION: LACTORACILLUS ACIDOPHILUS NUCLEIC ACIDS AND USES THEREOF
FILE REFERENCE: 035051/296336
CURRENT FILLING DATE: 2005-08-26
NUMBER OF SEQ ID NOS: 2561
SOFTWARE: Patentin version 3.2
SEQ ID NO 2174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLV--IPDEDY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 SMTWRLATYNNDLSGIINATCGVFLYDMDNIDDGSAFEIGFWRAFHKPVILVPFTNDPNK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 SMTWRLATYNNDLSGIINATCGVFLYDMDNIDDGSAFEIGFWRAFHKPVILVPFTNDPNK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 IYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVD---EHPEY--LH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 IYFGAGWFIDRQNKAYKEAMEALKENPIIDLENSYVPLDNQYKGIRVD---EHPEY--LH
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Best Local Similarity 32.5%; Pred. No. 2.3e-08;
Matches 49; Conservative 25; Mismatches 60; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 50; Length 167;
                                      ::: | :||| : ||: | : :| |:||: |: |
122 EKE--KGONLMIAQGUTTIIDGNTEFEKLADYNFNECPFNPVRG 163
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     115 DEDYCKPINLM-SWGVS---DNVIKMSQLKDFNFNKPRFDFYEG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.2%; Score 154.5; DB 5
Best Local Similarity 32.5%; Pred. No. 2.3e-08;
Matches 49; Conservative 25; Mismatches 60
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124 EKKMNLMIAQGUTTIIDGNTELEKLATYDFN 154
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Lactobacillus acidophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Lactobacillus acidophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-60-622-712-2174
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US-60-711-491-2174
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-60-622-712-2174
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Gaps

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RESULT 15
US-10-417-884A-6487
US-10-417-884A-6487, Application US/10417884A
; GENERAL INFORMATION:
; TILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TILE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 QEVYEKDMEELTNAEFVVAILDFEHQTIDPGTAYELGVATMLKKPMIIV---QEETVPTN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 IYFGAGWFIDRQNKAYKEAMEALKENPIIDLENSYVPLDNQYKGIRVDEHPEYLHDKVWA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 IYLAGPFFSEEQIDRVSRIEKALEENKTV--TSFYSPRHHQ-----ESNYELFSAGWA 64
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Best Local Similarity 23.0%; Pred. No. 0.28;
Matches 35; Conservative 28; Mismatches 74; Indels 15
                                                                                                                                                                                     NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESSE
ADDRESSEE: GRNOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <UNKNOWN>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/417,884A
FILING DATE: 17-APT-2003
PRIOR APPLICATION NUMBER: 05/98,598
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/051571
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
REFERENCE/COCKET NUMBER: GTC-012
TELEPHONE: (781)893-5077
TELEPHONE: (781)893-5077
TELEPHONE: (781)893-5077
TELEPHONE: (781)893-5077
TELEPHONE: CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acids
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TOPOLOGY: Innear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORIGINAL SOURCE:
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LOCATION: (B) LOCATION 1...156
US-10-417-884A-6487
                                                                                                                                                                                                                                                                                       CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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Search completed: December 23, 2005, 22:15:22 Job time : 572 secs

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December 23, 2005, 22:00:24 ; Search time 14 Seconds (without alignments) 118.825 Million cell updates/sec
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

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7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                     62187 segs, 10595856 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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848
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Perfect score:
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                                                                                             OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	Sequence 2176, Ap	Sequence 1678, Ap	Sequence 1742, Ap	326,	Sequence 404, App	464,	7	28,	Sequence 40, Appl	402,	Sequence 462, App	408,	Sequence 466, App		460,		Sequence 607, App	1152,	Sequence 2, Appli	285	287,	288,	289,	290,	291,
SOMMAKIES	ΩI	US-11-264-096-2176	US-60-732-162-1678	US-11-045-004-1742	US-10-556-060-326	US-60-732-162-404	US-60-742-219-464	US-11-288-493-44	US-10-244-081A-28	US-11-127-877A-40	US-60-732-162-402	US-60-742-219-462	US-60-732-162-408	US-60-742-219-466	US-60-732-162-406	US-60-742-219-460	US-11-238-031-5	US-11-045-004-607	US-11-045-004-1152	PCT-US05-20516-2	US-60-742-871-285	US-60-742-871-287	US-60-742-871-288	US-60-742-871-289	US-60-742-871-290	US-60-742-871-291
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ф	Query Match	10.0	9.6	8.7	8.6	8.5	8.5	8.5	8.5	8.3	8.3	8.3	8.3	8.3	8.3	8.3	8.3	8.2	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1
	Score	84.5	83	74	73	72.5	72.5	72.5	72	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	69.5	69	69	69	69	69	69	69	69
	Result No.	-	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Sequence 292, App Sequence 4, Appli Sequence 884, App	Sequence 509, App Sequence 511, App Sequence 510, App Sequence 286, App	Sequence 12, Appl Sequence 1782, Ap Sequence 2575, Ap	938	Sequence 9, Appli Sequence 9, Appli Sequence 6, Appli	Sequence 784, App Sequence 42, Appl Sequence 59, Appl Sequence 60, Appl
US-60-742-871-292 PCT-USO5-20516-4 US-60-742-219-884	US-60-742-871-509 US-60-742-871-511 US-60-742-871-510 US-60-742-871-286	US-11-170-482-12 US-11-045-004-1782 US-11-045-004-2575	US-11-045-004-938 US-60-733-588-11 US-60-733-434-11	US-60-733-588-9 US-60-733-434-9 PCT-US05-11978-6	US-60-732-162-784 US-60-741-048-42 US-60-742-872-59 US-60-742-872-60
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69 69	8 0 0 0 0 0 0	67 67 66.5	66.5 66.5 66.5	66.5 66.5 66.5	65.5 65.5 65.5
26 27 28	331,03	333 343 5	36 38	39 41 41	4444 9640

#### ALIGNMENTS

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251 GDRWILTAAHTIYPKDSVSLRKNQSVNVFLGHTAIDEMLKLGNHPVHRVVVHPDYRQNE- 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 396;
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10.0%; Score 84.5; DB 7; Length 39.
Best Local Similarity 23.1%; Pred. No. 0.072;
Matches 30; Conservative 26; Mismatches 49; Indels
                                           ATTLE OF INVENTION: Albumin Fusion Proteins FILE REPERENCE: PF546D1
CURRENT APPLICATION NUMBER: US/11/264,096
CURRENT APPLICATION NUMBER: 09/833,245
PRIOR PAPLICATION NUMBER: 09/833,245
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR PILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-14-25
NUMBER OF SEQ ID NOS: 2267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1678, Application US/60732162; GENERAL INFORMATION: APPLICANT: Belouchi, Abdelmajid APPLICANT: Raelson, John V
; Sequence 2176, Application US/11264096; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-11-264-096-2176
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US-60-732-162-1678
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29 KENPTIDLENSYVP----LDNQYKGIRVDEHPEYLHDKVWAT--ATYNNDLNGIKTNDIM 82
                                                                                                                  APPLICANT: KARST, UNE
APPLICANT: ENTIAN, KARL-DIETER
APPLICANT: HAUF, JORG
APPLICANT: ROSE, MATTHIAS
APPLICANT: VOSS, HAWIT
TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
FILE REFERENCE: 05394.0018-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33; Indels 18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 326, Application US/10556060
; GENERAL INFORMATION:
; APPLICANT: MEINKE, ANDREAS
; APPLICANT: HANNER, WARKUS
; APPLICANT: HANNER, WARKUS
; APPLICANT: HORKY, MARKUS
; APPLICANT: FALLENDA, SABINE
; APPLICANT: PROSTOMERSKY, SONJA
; TITLE OF INVENTION: S. AGALACTIAE ANTIGENS I + III
; FILE REFERENCE: SONN:0800US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 LGVYIPD------EEDVGLGM-ELGYALS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
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CURRENT PILING DATE: 2005-11-07
FRIOR APPLICATION NUMBER: PCT/EP2004/004856
FRIOR APPLICATION NUMBER: PCT/EP2004/004856
FRIOR FILING DATE: 2004-05-06
FRIOR FILING DATE: 2003-05-07
FRIOR APPLICATION NUMBER: 0345012.2
FRIOR APPLICATION NUMBER: 03450266.6
FRIOR PILING DATE: 2003-11-28
NUMBER OF SEQ ID NOS: 514
SEQ ID NO 326
LENGTH.1310
                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/11/045,004
CURRENT FILING DATE: 2005-01-28
FRIOR APPLICATION NUMBER: U0/637,657
FRIOR PILING DATE: 2003-08-11
FRIOR FILING DATE: 2003-08-11
FRIOR PILING DATE: 2002-10-08
FRIOR PILING DATE: 2002-10-08
FRIOR FILING DATE: 2001-04-11
FRIOR FILING DATE: 2000-04-11
FRIOR FILING DATE: 2000-04-11
FRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 2854
SEQ ID NO 1742
                        FRANCISCO
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                  GARCIA DEL PORTILLO, F
GOMEZ-LOPEZ, NURIA
MADUENIO, BNCARNA
PABLOS, BSTRIZ DE
WEHLAND, JURGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i LENGTH: 357
; TYPE: PRT
TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-1742
FERNANDO
BAQUERO,
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                                                                              APPLICANT: Croteau, Pascal
APPLICANT: Allard, Rene
APPLICANT: Allard, Rene
APPLICANT: Allard, Rene
APPLICANT: Berdewegh, Paul V
APPLICANT: Little, Randall D
APPLICANT: Keith, Tim
APPLICANT: Segal, Jonathan
TITLE OF INVENTION: Genemap of the Human Genes Associated With Asthma Disease
FILE REFERENCE: 059908-5010-PR
CURRENT APPLICATION NUMBER: US/60/732,162
CURRENT FILING DATE: 2005-11-02
NUMBER OF SEQ ID NOS: 4417
SOFTWARE: PatentIn version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 DRQNKAYKEAMEALKE--NPTIDL------ENSYVPLDNQ-YKGIRVDEHPEYLHD 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.8%; Score 83; DB 8; Length 3354;
22.2%; Pred. No. 1.9;
tive 32; Mismatches 68; Indels
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TIERREZ-MARTINEZ, ALBERTO
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CHARBIT, ALAIN
DURANT, LIONEL
PEREZ-DIAZ, JOSE-CLAUDIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAZQUEZ-BOLAND, ANTONIO
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APPLICANT: FRANGEUL, LIONEL
APPLICANT: COUVE, ELISABETH
APPLICANT: RUSNIOK, CHRISTOPHE
APPLICANT: FSIHI, HAPIDA
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CHAKRABORTY, TRINAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEHOUX, PIERRE
DUSSURGET, OLIVIER
CHETOUANI, FARID
                                          Fournier, Helene
Nguyen-Huu, Quynh
Croteau, Pascal
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Bradley, Walter E
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GLASER, PHILIPPE
KUNST, FRANCK
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GOEBEI, WERNER
KREFT, JURGEN
KUHN, MICHAEL
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Best Local Similarity 22.2*
Matches 36; Conservative
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HAIN, THORSTEN
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homosapiens
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LENGTH: 3354
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US-11-288-493-44
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APPLICANT: Groteau, Pascal
APPLICANT: Allard, Rene
APPLICANT: Allard, Rene
APPLICANT: Berdewegh, Paul V
APPLICANT: Berdewegh, Paul V
APPLICANT: Little, Randall D
APPLICANT: Segal, Jonathan
TITLE OF INVENTION: Genemap of the Human Genes Associated With Asthma Disease
FILE REPERENCE: 05908-5010-9R
CURRENT APPLICATION NUMBER: US/60/732,162
CURRENT FILING DATE: 2005-11-02
                 3;
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                                                                                                                              96 GMELGYALSQGKYVLLVIPDEDYGKPINLMSWGV---SDNVIKMSQLKDFNFNKPRFD 150
                                                                                                                                                       ----YLHDKVWATATYNNDLNGIKTNDIMLGVYIPDEED
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                                                     ---NGIKTNDIMLGVYIPDEEDVGL-
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                 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 -GGGSRSGVRLEDFNYNNQTITDQIY-RAMNSSSFEGVSGHVV 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 VGLGMELGYALSQGKYVLLVIPDEDYGKPINLMSW-GVSDNVI 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.5%; Score 72.5; DB 8;
Best Local Similarity 23.9%; Pred. No. 2.6;
 22.9%; Pred. No. 6.9; ive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Mismatches
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APPLICANT: Belouchi, Abdelmajid
APPLICANT: Bradley, Walter Edward
APPLICANT: Bradley, Walter Edward
APPLICANT: Paquin, Bruno
APPLICANT: Nguyen-Huu, Quynh
APPLICANT: Croteau, Pascal
APPLICANT: Allard, Rene
APPLICANT: Little, Randall David
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                                                                                                                                                                                                                                                          ; Sequence 404, Application US/60732162
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Eerdewegh, Paul Van
                                                                                                                                                                                                                                                                                            APPLICANT: Belouchi, Abdelmajid
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SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                Raelson, John V
Bradley, Walter E
Paguin, Bruno
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                                                                                                                                                                                                                                                                                                                                                                       Fournier, Helene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Conservative
                 27; Conservative
                                                     61 DKVWATATYNNDL-
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ORGANISM: Homosapiens
Similarity
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US-60-732-162-404
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LENGTH: 578
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 Best Local
Matches 2
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GENERAL INFOGRATION:

APPLICANT: Kelly, Louise M.
APPLICANT: Earzoll, Joseph M.
APPLICANT: Farlow, Deborah M.
APPLICANTON: HERMINGS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: 141742, 17622, 21689, 28899, 36894, 6369, 6369, 6469, 21804, 2918, 21804, 941, 2061, 5891, TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21804, 2917, 2061, 5891, TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21804, 941, 2061, 1171E OF INVENTION: 5014
TITLE OF INVENTION: 5014
PRIOR PELLIKG DATE: 2003-02-05
PRIOR PELLIKG DATE: 2003-02-05
PRIOR PELLIKG DATE: 2003-02-05
PRIOR PELLIKG DATE: 2003-04-03
PRIOR PELLIKG DATE: 2003-04-03
PRIOR PELLIKG DATE: 2003-04-03
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PRIOR PELLIKG DATE: 2003-04-03
PRIOR PELLIKG DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US 60/450, 279
PRIOR PELLIKG DATE: 2003-04-03
PRIOR PELLIKG DATE: 2003-04-03
PRIOR PELLIKG DATE: 2003-04-04
PRIOR PELLIKG DATE: 2003-04-04
PRIOR PELLIKG DATE: 2003-04-04
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PRIOR PELLIKG DATE: 2003-04-04
PRI
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APPLICANT: Segal, Jonathan
TITLE OF INVENTION: Gene Map of the Human Genes Associated with Psoriasis FILLE REPERENCE: 305522-205
CURRENT APPLICATION NUMBER: US/60/742,219
CURRENT FILING DATE: 2005-12-05
NUMBER OF SEQ ID NOS: 7303
SOFTWARE: PatentIn version 3.3
SEQ ID NO 464
LENGTH: 578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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NUMBER OF SEQ ID NOS: 80
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8.5%; Score 72.5; DE
Best Local Similarity 23.9%; Pred. No. 2.6;
Matches 39; Conservative 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 44, Application US/11288493 GENERAL INFORMATION:
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US-60-742-219-464
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TYPE: PRT
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Sequence 40, Application US/11127877A

GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Laenen, Wendy
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
                                                                                                                        13;
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                                                                                                                                                                                       51 RVDEHPEYLHDKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVL 110
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                                                                                                                                                                                                                                                                                                                                               111 LVIPDEDYGKPINLM-----SWGVSDNVIKMSQLKDFNFNKPRFDFY--EGAVY 157
                                                                                                                                                              9 GAGWFTDRQNKAYKEAMEALKENPTIDLE--------NSYVPLDNQYKGI
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                                                                                                                        51;
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                                                                               8.5%; Score 72.5; DB 7; Length 710; 26.0%; Pred. No. 3.4;
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APPLICANT: Gerard, Gary
APPLICANT: Gerard, Gary
APPLICANT: Grandilya, Harini
APPLICANT: Griffiths, Katherine Rachel
APPLICANT: Gibbs, Moreland David
APPLICANT: Gibbs, Moreland David
APPLICANT: Bergquisht, Peter Leonard
APPLICANT: Bergquisht, Peter Leonard
APPLICANT: Bergquisht, Peter Leonard
APPLICANT: Bergguisht, Peter Leonard
APPLICANT: David Now Polymerases and Mutants Thereof
FILE REPERENCE: 0942.5360001
CURRENT APPLICATION NUMBER: US/10/244,081A
CURRENT APPLICATION NUMBER: US 60/318,903
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 60/318,903
PRIOR FILING DATE: 2001-09-14
SOFTWARE: PALENTIN Version 3.1
SEQ ID NO 28
LENGTH: 893
                                                                                                                        54; Indels
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                                                                                                                    26; Mismatches
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24.1%; Pred. No.
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ORGANISM: Thermatoga neopolitina
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Matches 39; Conservative
                                                                                                                      46; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-288-493-44
                                                                             Query Match
Best Local Similarity
Matches 46; Conserva
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APPLICANT: Debrus, Sophie
APPLICANT: Debrus, Sophie
APPLICANT: Exclewegh, Paul V
APPLICANT: Little, Randall D
APPLICANT: Keith, Tim
APPLICANT: Segal, Jonathan
TITLE OF INVENTION: Genemap of the Human Genes Associated With Asthma Disease
FILE REFERENCE: 059908-5010-PR
CURRENT APPLICATION NUMBER: US/60/732,162
CURRENT FILING DATE: 2005-11-02
NUMBER OF SEQ ID NOS: 4417
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.3%; Score 70.5; DB 7; Length 844; Best Local Similarity 23.9%; Pred. No. 7.1; Matches 39; Conservative 20; Mismatches 51; Indels 5.
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TITLE OF INVENTION: Amyloid-Beta Protein Production
              CURRENT APPLICATION NUMBER: US/11/127,877A
CURRENT PELING DATE: 2005-05-12
PRIOR FILING DATE: 2005-05-12
PRIOR FILING DATE: 2004-05-12
PRIOR FILING DATE: 2004-06-12
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SEQ ID NO 40
LENTH: 844
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APPLICANT: Raelson, John V
APPLICANT: Bradley, Walter E
APPLICANT: Paquin, Bruno
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SEQ ID NO 402
LENGTH: 844
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Croteau, Pascal
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US-11-127-877A-40
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US-60-732-162-402
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Best Local Similarity
Matches 39; Conserv
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US-60-742-219-466
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US-60-732-162-406
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APPLICANT: Berdewegh, Paul V
APPLICANT: Estewegh, Paul V
APPLICANT: Little, Randall D
APPLICANT: Keith, Tim
APPLICANT: Segal, Jonathan
TITLE OF INVENTION: Genemap of the Human Genes Associated With Asthma Disease
FILE REFERENCE: 059908-5010--R
CURRENT APPLICATION WUMBER: US/60/732,162
CURRENT FILING DATE: 2005-11-02
NUMBER OF SEQ ID NOS: 4417
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                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Segal, Jonathan
TITLE OF INVENTION: Gene Map of the Human Genes Associated with Psoriasis
FILE REPERBERGE: 306522-2000
CURRENT APPLICATION NUMBER: US/60/742,219
CURRENT FILING DATE: 2005-12-05
NUMBER OF SEQ ID NOS: 7303
SOFTWARE: Patentin version 3.3
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93 VGLGMELGYALSQGKYVLLVIPDEDYGKPINLMSW-GVSDNVI 134
                                                                                                                                                            APPLICANT: Belouchi, Abdelmajid
APPLICANT: Braelson, John Verner
APPLICANT: Bradley, Walter Edward
APPLICANT: Paquin, Bruno
APPLICANT: Oguyen-Huu, Quynh
APPLICANT: Croteau, Pascal
APPLICANT: Allard, Rene
APPLICANT: Allard, Rene
APPLICANT: Allard, Rene
APPLICANT: Allard, Rene
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GENERAL INFORMATION:
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APPLICANT: Raelson, John V
APPLICANT: Bradley, Walter E
APPLICANT: Paquin, Bruno
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Eerdewegh, Paul Van
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Nguyen-Huu, Quynh
Croteau, Pascal
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US-60-742-219-462
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LENGTH: 844
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TITLE OF INVENTION: Gene Map of the Human Genes Associated with Psoriasis
FILE REPERENCE: 306522-2000
CURRENT APPLICATION NUMBER: US/60/742,219
CURRENT FILING DATE: 2005-12-05
NUMBER OF SEQ ID NOS: 7303
SOFTWARE: PatentIn version 3.3
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                                                                                                                                                                                             51; Indels
                                                                                                                                                                                                                                    3 KKTIYFGAGWFTDRQNKAY-----KEAMEALKENPTIDL----
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                                                                                                                                                    8.3%; Score 70.5; DE 23.9%; Pred. No. 7.8; tive 20; Mismatches
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APPLICANT: Bradley, Walter Edward
APPLICANT: Bradley, Walter Edward
APPLICANT: Paquin, Bruno
APPLICANT: Oguyen-Huu, Quynh
APPLICANT: Allard, Rene
APPLICANT: Allard, Rene
APPLICANT: Little, Randall David
APPLICANT: Kelth, Tim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 466, Application US/60742219 GENERAL INFORMATION:
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Eerdewegh, Paul Van
SOFTWARE: PatentIn version 3.3 SEQ ID NO 408 LENGTH: 899
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Best Local Similarity 23.9%
Matches 39; Conservative
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Best Local Similarity 23.9%
Matches 39; Conservative
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                                                             TYPE: PRT
ORGANISM: Homosapiens
US-60-732-162-408
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                                         Jebrus, Sophie

Jebrus, Sophie

Jettle, Randall D

APPLICANT: Eerdewegh, Paul V

APPLICANT: Little, Randall D

APPLICANT: Keith, Tim

APPLICANT: Segal, Jonathan

TITLE OP INVENTION: Genemap of the Human Genes Associated With Asthma Disease

FILE REFERRNCE: 059908-5010-PR

CURRENT APPLICATION NUMBER: US/60/732,162

CURRENT FILING DATE: 2005-11-02

NUMBER OF SEQ ID NOS: 4417

SOPTWARE: Patentin version 3.3

SEQ ID NO 406

LENGTH: 961

TYPE: no...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KKTIYFGAGWFTDRQNKAY-----KEAMEALKENPTIDL------ENSYV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Segal, Jonathan TITLE OF INVENTION: Gene Map of the Human Genes Associated with Psoriasis FILLE REFERENCE: 306522-2000
CURRENT APPLICATION NUMBER: US/60/742,219
CURRENT FILING DATE: 2005-12-05
NUMBER OF SEQ ID NOS: 7303
SOFTWARE: Patentin version 3.3
SEQ ID NO 460
LENGTH: 961
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23.9%; Pred. No. 8.5;
tive 20; Mismatches 51; Indels 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - GGGGRSGVRLEDFNYNNQTITDQIY-RAMNSSSFEGVSGHVV 526
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8.3%; Score 70.5; DE
Best Local Similarity 23.9%; Pred. No. 8.5;
Matches 39; Conservative 20; Mismatches
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APPLICANT: Raelson, John Verner
APPLICANT: Bradley, Walter Edward
APPLICANT: Paquin, Bruno
APPLICANT: Nguyen-Huu, Quynh
APPLICANT: Allard, Rene
APPLICANT: Little, Rene
APPLICANT: Little, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 460, Application US/60742219 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cousineau, Johanne
Eerdewegh, Paul Van
Belouchi, Abdelmajid
                   John V
Walter E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 23.99
Matches 39; Conservative
                   Raelson, John V
Bradley, Walter
Paquin, Bruno
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ORGANISM: Homo sapiens
US-60-742-219-460
                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homosapiens
US-60-732-162-406
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US-60-742-219-460
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Gaps

53;

51; Indels

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-- 485
---ENSYV 41
                                                         -- YLHDKVWATATYNNDLNGIKTNDIMLGVYIPDEED
---KEAMEALKENPTIDL----
                                                                            93 VGLGMELGYALSQGKYVLLVIPDEDYGKPINLMSW-GVSDNVI 134
                                                                                                                                                                                          Search completed: December 23, 2005, 22:17:35
Job time : 15 secs
 3 KKTIYFGAGWFTDRQNKAY----
                                                        42 PLDNOYKGIRVDEHPE
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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sw model protein search, using OM protein Run on:

December 23, 2005, 21:50:25 ; Search time 38 Seconds (without alignments) 397.527 Million cell updates/sec

Title: Perfect sc Sequence:

US-10-049-750-14 848 1 MPKKTIYFGAGWFTDRQNKA......QLKDFNFNKPRFDFYEGAVY 157 score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	nucleoside deoxyri	hypothetical prote	Ig light chain-bin	amine oxidase (cop	conserved hypothet	maturase-related h	hypothetical prote	cag island protein	RAS GTPase-activat	VP1 protein - porc	c	cag pathogenicity	probable ATP-depen		cathepsin L (EC 3.	acetyl-CoA carboxy	hypothetical prote	chitinase family p	DNA polymerase III	hypothetical prote	conserved hypothet	hypothetical prote	neprilysin (EC 3.4	hypothetical prote	DNA topoisomerase	hypothetical prote	inner layer protei		hypothetical prote
SUMMAKIES		JC7522	E86686	A42808	G90330	A86717	B28439	F84113	G71925	A40258	839261	A42091	A64587	T00936	H95078	847433	S63347	T17774	H97091	A97323	H85435	E69936	C84827	HYRBN	A71006	C83917	878398	PIXRBR	S13558	T18444
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	Query Match	75.1	16.1	10.7	10.7	10.2	9.8	9.8	9.7	9.7	9.7	7.6	9.6	9.6	9.6	9.6	9.5	9.4	9.4	9.4	9.3	٠	•	9.5	9.5	9.1	9.1	9.1	9.1	9.1
	Score	637	136.5	91	90.5	86.5	83	83	82.5	82.5	82	82	81.5	81.5	81	81	80.5	80	79.5	79.5	78.5	78.5	78	78	78	77.5	77.5	77	77	77
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hypothetical prote	proline-tRNA ligas	aspartyl-tRNA synt	immunoglobulin-bin	P60 protein - oat	rhoptry protein -	thymidine kinase (	thymidine kinase (	hypothetical prote	hypothetical prote	probable TonB-depe	hypothetical prote	hypothetical prote	hypothetical prote	FK506 polyketide s	hypothetical prote
E64476	G71695	H75443	A45063	S45723	T28677	KIVZSW	KIVZSK	D89769	B98074	AB0124	T00153	I64233	H89984	T17426	E64464
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241	432	435	455	519	2269	177	181	256	437	9	759	1177	1260	1504	602
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76.5	76.5	26	92	92	92	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

		2.4.2.6) II - Lactobacillus helveticus
		oside deoxyribosyltransferase (EC 2.4.2.6) II - I
T 1	7	oside

C;Species: Lactobacilius helveticus
C;Species: Lactobacilius helveticus
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004
C;Accession: JG7522; PC7103
R;Okuyama, K.; Noguchi, T.
Biosci. Biotechnol. Biochem. 64, 2243-2245, 2000
Biosci. Biotechnol. Biochem. 64, 2243-2245, 2000
A;Title: Molecular cloning and expression of the nucleoside deoxyribosyltransferase-II of the number: JG7522; MUID:21012342; PMID:11129605

A;Gene: ndtB C;Keywords: glycosyltransferase; pentosyltransferase

ö Gaps .; 0 Query Match 75.1%; Score 637; DB 2; Length 158; Best Local Similarity 73.5%; Pred. No. 8.9e-49; Matches 114; Conservative 21; Mismatches 20; Indels

62 3 KKTIYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDK

63 4 KKTLYFGAGWFNEKQNKAYKEAMAALKENPTVDLENSYVPLENQYKGIRIDEHPEYLHNI ò 셤 63 VWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPI 122 ò

123 NLMSWGVSDNVIKMSQLKDFNFNKPRFDFYEGAVY 157

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124 ILMSWGVCDNASQISELKDFDFNKPRYNFYDGAVY 158 셤

hypothetical protein yejD [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004

C;Accession: E86686

R.Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. 11, 731-753, 2001 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s' A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: E86686

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264 NQDGIAKALAYYG----LIHYSVEKDFVS----KDQNFNKVK-DFH 300
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218 FTLDQVMCFGDSENDLTMI
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                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: G90330
A; Status: preliminary
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A;Cross-references: UNIPROT:Q51912; UNIPARC:UPI000017ABEA; GB:W86697
A;Kastern, W.; Holst, E.; Nielsen, E.; Sjoebring, U.; Bjoerck, L.
A;Kastern, W.; Holst, E.; Nielsen, E.; Sjoebring, U.; Bjoerck, L.
A;Title: Protein L, a bacterial immunoglobulin-binding protein and possible virulence de A;Reference number: A41493; MUID:90215984; PMID:2108927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A42808
Ig light chain-binding protein precursor - Peptostreptococcus magnus
Nyllermate names is protein L
C;Alternate names protein L
C;Species: Peptostreptococcus magnus
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
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C;Date: 19-May-1994
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                                        A,Molecule type: DNA A,Rolecule type: DNA A,Rolecule type: DNA A,Rolecule type: DNA A,Rolecule type: 1-159 <STO>
A,Rolecule to the A,Colecule to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the total to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLHDKVWATATYNNDL----NGIKTNDIML---GVYIPDEEDVGLGMELGYALSQGKYV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 ----WATATYNNDLNGIKTNDIMLGVYIPDEEDV--GLGMELGYALSQGKYVLLVIPDED 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G90330 amine oxidase (copper-containing) (tynA) [imported] - Sulfolobus solfataricus (Species: Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 IYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDKV--
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                                                                                                                                                                                                                                                                                                                                                                                      16.1%; Score 136.5; DB 2; Length 159; 26.7%; Pred. No. 6.9e-05; tive 34; Mismatches 57; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.7%; Score 91; DB 2; Length 719; Best Local Similarity 28.0%; Pred. No. 4.5; Matches 37; Conservative 17; Mismatches 50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 YGKPINLMSWGVSDN----VIKMSQLKDFNFNKPRFDFYEG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 202-275 <KA2>
A;Cross-references: UNIPARC:UPI000017ABEB
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43; Conservative
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Best Local Similarity
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A;Status: preliminary
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: G90330
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Vong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Parett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-660 <KUR>
A;Cross-references: UNIPROT:Q97XM1; UNIPARC:UP100000687EB; GB:AE006641; NID:g13814942; P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conserved hypothetical protein yheD [imported] - Lactococcus lactis subsp. lactis (strain C) bate: 3.7 Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004 ().7 Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004 ().7 Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004 ().7 Marchan, A.; Whicker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlin R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, M.; Weissenbach, J.; Ehrlin A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A;Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Cross-references: UNIPROT.Q9CHJ4; UNIPARC:UPI0000C68CE; GB:AE005176; PID:g12723652; P
A.Experimental source: strain IL1403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 PPITLDERGE-----CEKAVRNDKRVQEALTKRGILINDLNLLMVDCWAPGHVDEELR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 GLGMELGYALSQGKYVLLVIPDEDYGKPIN-LMSW------GVSDNVIKMSQLKDFN 143
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10.7%; Score 90.5; Di
Best Local Similarity 26.5%; Pred. No. 4.5;
Matches 48; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Gene: tynA
C, Superfamily: amine oxidase (copper-containing)
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A, Status: preliminary
A, Molecule type: DNA
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maturase-related hypothetical protein RF2 - yeast (Saccharomyces cerevisiae) mitochondrial maturase-related hypothetical protein RF2 - yeast (Saccharomyces cerevisiae)
C;Species: mitochondrion Saccharomyces cerevisiae
A;Variety: Saccharomyces uvarum
C;Date: 28-Aug-1989 #text_change 09-Jul-2004
C;Accession: B28439
R;Seraphin, B.: Simon, M.; Faye, G.
J. Biol. Chem. 262, 10146-10153, 1987
A;Title: The mitochondrial reading frame RF3 is a functional gene in Saccharomyces uvaru
A;Reference number: A92597; MUID:87280035; PMID:2440860
A;Accession: B2849
A;Molecule type: DNA
A;Residues: 1-101;102-206 <SER>
A;Cross-references: UNIPROT:Q7M2B0; UNIPARC:UP10000093B37; UNIPARC:UP1000017B3A7
A;Cross-references: UNIPROT:Q7M2B0; UNIPARC:UP10000013B37; A;Genetics:
A;Genetics:
A;Genetics:
A;Genetic code: SGC2
C;Keywords: mitochondrion
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C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F84113
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Recence number: A83550; MUID:20512582; PMID:11058132
A;Recence number: A83550; MUID:20512582; PMID:11058132
A;Residues: J-569 cSTO-A;Residues: 1-369 cSTO-A;Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KGHNFMLKLDELSNS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 GDGYFGIKKOMTHSFNI-TLKKYDIITLENIKYYLNLTSKIYVDNKYNKVQ-----LH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.8%; Score 83; DB 2; Length 206; Best Local Similarity 21.8%; Pred. No. 4.7; Matches 36; Conservative 28; Mismatches 51; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 TK-WFSTKYINFIAFMALEIIIKGLYHTD-
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cag island protein - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: G71925
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: G71925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9ZLU1; UNIPARC:UPI00000D363E; GB:AE001482; GB:AE001439; NID C;Genetics:
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Accession: A40258; A56606, T40588
R;Imai, Y.; Miyake, S.; Hughes, D.A.; Yamamoto, M.
Mol. Cell. Biol. 11, 3088-3094, 1991
A;Title: Identification of a GTPase-activating protein homolog in Schizosaccharomyces po A;Reference number: A40258; MUID:91246176; PMID:2038319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule_type: DNA,
Mseaidues: 1-76 < MNN.
A;Residues: 1-76 < MNN.
A;Residues: 1-76 < MNN.
A;Cross-references: UNIPARC:UPI000012B0D2; GB:S37449; NID:G234782; PIDN:AAB19697.1; PID
A;Note: sequence extracted from NCBI backbone (NCBIN:106678, NCBIP:106679)
A;Note: sequence extrais, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A;Reference number: 221938
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:P33277; UNIPARC:UP1000012B0D2; GB:D10457; NID:g218534; PIDN
R;Wang, Y.; Boguski, M.; Riggs, M.; Rodgers, L.; Wigler, M.
A;Wang, Y.; Boguski, M.; Riggs, M.; Rodgers, L.; Wigler, M.
A;Hile: sarl, a gene from Schizosaccharomyces pombe encoding a protein that regulates :
A;Reference number: A56606; MUID:91355280; PMID:1883874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: UNIPARC:UP100012B0D2; EMBL:AL035216; PIDN:CAA22816.1; GSPDB:GN0006 A; Experimental source: strain 972h-; cosmid c646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 NGIKTND---IMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPI-NLMSWGV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 QNKAYKEAMEALKENPTID--LENSYVPLDNQYKGIRVD-EHPEYLHDKVWATATYNNDL 73
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9.7%; Score 82.5; DE
Best Local Similarity 26.0%; Pred. No. 11;
Matches 38; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 LDNIDYYLQLERNKFDSKAKDIAQKA 242
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probable ATP-dependent RNA helicase At2g42270 [imported] - Arabidopsis thaliana N;Alternate names: ATP-dependent RNA helicase homolog T24P15.18 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004 C;Accession: T00936; H84851 R;Reunsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
sequence extracted from NCBI backbone (NCBIN:82354, NCBIP:82360)
A;Note: sequence ext
C;Genetics:
A;Gene: FlyBase:brm
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Accession: A42091
R;Tamkun, J.W.; Deuring, R.; Scott, M.P.; Kissinger, M.; Pattatucci, A.M.; Kaufman, T.C.
Call 68, 561-57, 1992
A;Title: brahma: a regulator of Drosophila homeotic genes structurally related to the year Reference number: A42091; MUID:92154670; PMID:1346755
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-1638 < TAM>
A; Cross-references: UNIPROT: P25439; UNIPARC: UPI000016BB03; GB: M85049; NID: 9157011; PIDN: A; Experimental source: iso-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: S39261
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1088 <ALMA
A;Cross-references: UNIPROT:Q85036; UNIPARC:UPI000061936; EMBL:X76486; NID:g434312;
C;Superfamily: rotavirus inner layer protein VP1
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                                                                                                                                                                                                                                                                                                              ---FNFNKPRFDFYEGAV 156
                                                                                                                                                                                                                                                                                                                                    ---DLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIP 114
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                                                                                                                                                                          562 AIELLDELSTLRLVDKENRYEPLTSEVEKEFIDLDALYERIRAERDALQDVHRAICDHNE 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: porcine rotavirus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S39261
R;Almanza, L.; Arias, C.F.; Lopez, S.
submitted to the RMBL Data Library, November 1993
A;Description: Aminoacid sequence of the Porcine rotavirus YM VP1 protein.
A;Reference number: S39261
                                                                                                                                 24 AMEALKENPT---IDLENSYVP-----EHPE
                                                                                                                                                                                                                                                                   ---SKGFSRGVGVVGI----
                                                                                          Gaps
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  F;154-398/Domain: ras-specific GAP catalytic domain homology <GAP>
                                             DB 2; Length 766;
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                                                                                        43; Indels
                                                                                                                                                                                                                                                              622 YLQTQLQIYGSYLNNARSQIK------PSHSD---
                                                                                                                                                                                                                                                                                                           117 DYGKPINLMSWGVSDNVIKMS--QLKD------
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20.6%; Pred. No. 47;
tive 30; Mismatches 43
                                                                                      17; Mismatches
                                           9.7%; Score 82.5; 1
25.4%; Pred. No. 27;
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                                                                                        46; Conservative
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                                                                 Best Local Similarity
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Matches
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839261
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C;Accession: A64587
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Feterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne, son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: A64587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 LG------EDYGEDVGLGMELGYALSQGKYVLLV----IPD-----EDYGKPINL 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       744 --RTBEQTYYSIAHTIHEKVVEQASIMVNGTLKEYQIKGLEWLVSLYNNNLNGILADEMG 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----WATATYNNDLNGIKTNDIM 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Species: Helicobacter pylori
C,Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cag pathogenicity island protein cag16 - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                   88 WIDDEEDSCGSNDDHKPKVE---EQPTATEDATDKAQATGNDEDAKDLITKAKVEDDEY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 QNKAYKEAMEALKENPTID--LENSYVPLDNQYKGIRVD-EHPEYLHDKVWATATYNNDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                 Length 1638;
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                                                                                                                                                                                                                                                          Indels
A;Cross-references: FlyBase: FBgn0000212
C;Superfamily: human SNF2alpha protein; bromodomain homology
C;Keywords: transcription regulation
F;1451-1506/Domain: bromodomain homology <BRO>
                                                                                                                                                                                                                                                              46;
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9.6%; Score 81.5; DE
Best Local Similarity 25.3%; Pred. No. 14;
Matches 37; Conservative 23; Mismatches
                                                                                                                                                              Query Match
Best Local Similarity 20.2%; Prec. ....
Marches 41; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 SDNVIKMSQLKDFNFNKPRFDFYEGA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDNIDYYLÓLERNKFDSKAKDIAQKA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 GIRVDEHPEY----LHDKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 MSWGVSDNVIKM--SQLKDFNFN 145
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C;Accession: 847433
R;le Boulay, C.; van Wormhoudt, A.; Sellos, D.
Ribe Boulay, C.; van Wormhoudt, A.; Sellos, D.
Rybescription: Molecular Library, August 1994
A;Description: Molecular cloning and sequencing of the two cDNAs that encode cathepsin L.
A;Reference number: 847432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:Q27708; UNIPARC:UPI0000084019; EMBL:X80990; NID:g530735; PID
   109 LLLTDNGPLGFQLLHPQYHVDK-----TYQVEVNGLLTPDHIQTFQKGIVFLDDTVCKPA 163
                                                                                                        --EDVGLGMELGYA---LSQGKYVLLVIPDEDYGKPINLMSWGVSDNVIKMSQLKDFNFN 145
                                                                                                                                                                 164 KLEILSASPSLSQASITISEGKFHQI-----KKM-FLSVGVKVTSLKRIQFGDFTLN 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 HTEEALHEAV-----SDIGPISVAIDASHFSFQFYSSGVYYEKKCSPTNLDHGV-LAV 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 H-PRYLHDKVWATATYNNDLNGIKT-----NDIMLGVYI----PDEEDVGLGMEL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                              cathepsin L (EC 3.4.22.15) - Norway lobster
C;Species: Nephrops norvegicus (Norway lobster)
C;Date: 23-Nov-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 GYALSQGKYVLLVIPDEDYGKPINLMSWGV---SDNVIKMSQLKDFN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 GYGTES-----TEDYWLVKN--SWGSGWGDAGYIKMSRNRDNN 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 GAGWFTDRONKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Kerwords: cysteine proteinase; hydrolase
F;122,260,280/Active site: Cys, His, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.6%; Score 81; DB; Best Local Similarity 26.3%; Pred. No. 12; Matches 44; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: December 23, 2005, 22:04:55
Job time : 42 secs
                                                                                                                                                                                                                                       146 KPRFDFYEG 154
                                                                                                                                                                                                                                                                                                215 P---DLAEG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-313 <LEB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: papain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S47433
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H95078
hypothetical protein SP0680 [imported] - Streptococcus pneumoniae (strain TIGR4)
c;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: H95078
R;Tettelin, H.; Nelson, K.B.; Paulsen, I.T.; Bisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A95000; MUD:21357209; PMID:11463916
A;Accession: H95078
A;Status: preliminary
A;Molecule type: DNA
A;Residues 1-241 KCMR>
A;Cross-references: UNIPROT:097RV6; UNIPARC:UP1000005153B; GB:AE005672; PIDN:AAK74825.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene SP0680
C;Superfamily: conserved hypothetical protein H11243
submitted to the EMBL Data Library, December 1997
A; Description: Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence.
A; Accession: T00936
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-2172 < ROU'S
A; Status: translated from GB/EMBL/DDBJ
A; Rosidues: 1-2172 < ROU'S
A; Cross-references: UNIPROT: O48534; UNIPARC: UPI00000AB148; EMBL: AC002561; NID: G2673901;
A; Experimental source: cultivar Columbia
R; Lin, X; Kaul, S:; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487; PMID: 10617197
A; Accession: H84851
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1621, M., 1623-2172 <STO>
A; Cross-references: UNIPARC: UPI000017AF4A; GB: AE002093; NID: G2673917; PIDN: AAB88651.1; G
C; Genetics:
A; Map posttion: 2
A; Map posttion: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435 MDLESLAFNQGGFTRENNKC--ELPDRSFRIRGKEFDEVHVPWVSKKFDSNEKLVKISDL 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        493 PEWAQPAFRGMQQLNRVQSKVYGTALFKADNILLCAPTGAGKTNVAVLTIL----HQLGL 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MPKKTIYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVP----LDNQYKGIRVDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEY-------LHDKVWATATYNND-----LNGIKTNDIMLGVYIPDEEDVGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

9.6%; Score 81.5; DB 2; Length 2172;
Best Local Similarity 23.2%; Pred. No. 1.38+02;
Matches 39; Conservative 27; Mismatches 61; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 GMELGYALSQGKYVLLVIPDEDYGKPINLMSWGVSDNVIKMSQ-LKDF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 9.6%; Score 81; DB 2; Length 241; l Similarity 24.9%; Pred. No. 8.5; 47; Conservative 19; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Si
Matches 47,
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Gaps

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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sw model using - protein search, protein Š December 23, 2005, 21:48:35; Search time 230 Seconds (without alignments) 481.600 Million cell updates/sec Run on:

US-10-049-750-14 848 Title:

score: Perfect sc Sequence:

1 MPKKTIYFGAGWFTDRQNKA.....QLKDFNFNKPRFDFYEGAVY 157

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2166443 Total number of hits satisfying chosen parameters:

2166443 segs, 705528306 residues

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1	Q8rly4 lactobacill									Q4qay0 leishmania					Q7p6v5 fusobacteri	Q415e4 staphylococ				_				_				_	4	Q9h804 homo sapien
SUMMARIES	ID	NTD LACLE	Q8RLY4 LACHE	QSFMM8_LACAC	NTD LACTO	Q9KWF0_LACHE	NTD LACFE	Q8RLYS_LACHE	Q5FINO_LACAC	Q9CI73_LACLA	Q88SL4_LACPL	Q4QAYO_LEIMA	Q88X23_LACPL	Q9EMRO AMEPV	QSZMQ1_CHICK	Q4Z0Q6_PLABE	Q7P6V5_FUSNV	Q4L5E4_STAHJ	ADEC METAC	Q51912_PEPMA	Q97XM1_SULSO	Q4JUB7_CORJK	Q8RHH4_FUSNN	Q7WST1_PSEPA	Q7R989_PLAYO	Q7RKP6_PLAYO	AMPA CANBF	Q7PSF2 FUSNV	Q7RT73_PLAYO	Q8TMR7_METAC	Q9CHJ4_LACLA	Q9H804_HUMAN
	th DB	156 1	158 2	159 2	49 1	.58 2	89	167 2				-	-	149 2																678 2		138 2
	Length																														7	
de	Query	9.66	85.8	84.8	77.	74.8	24.	20.2	18.	16								10.	10.	10.	10.	10.	10.	10.	10.	10.	10.	10.	10.3	10.	•	10.
	Score	843	728	719	653	634	209	171.5	154.5	136.5	124.5	106	96	96	95	93.5	93.5	92.5	92	91	90.5	90	89	89	89	89	88	88	87.5	87		85.5
	Result No.	-	7	e	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

Q9nzp8 homo sapien Q5ffg8 ehrlichia r Q7mqx8 wolinella s Q6llu3 photobacter Q91yr4 mus musculu Q8btx6 mus musculu Q6pgb brachydanio Q7vb88 prochloroco Q4uas6 theileria a Q4ud66 theileria a Q4ud66 theileria a Q895m8 clostridium Q5bbx6 ehrlichia r	Q8n5r0 homo sapien
Q9NZPB HUMAN TIG EHRG Q7MQXB WOLSU BTUB PHOPR Q91YT4 MOUSE SKZLZ MOUSE SKZLZ MOUSE Q6P9PZ BRARE Q7VB8B PROMA Q4UASG THEAN Q4UBS THEAN Q89SMB CLOTE	Q8N5R0_HUMAN
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487 446 480 606 725 993 1040 1568 154 2985 3091 351	296
100.00 100.00 100.00 100.00 100.00	9.9
8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9	84
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## ALIGNMENTS

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                  X-AX CRYSTALLOGRAPHY (2.4 ANGSTROMS).
MEDLINE=96419140; PubMed=8805514;
Armstrong S.R., Cook W.J., Short S.A., Ealick S.B.;
Armstrong S.R., Cook W.J., Short S.A., Ealick S.B.;
Armstrong S.R., Cook W.J., Short S.A., Ealick S.B.;
and ligand-bound forms reveal architecture of the active site.";
Structure 4:97-107(1996).
-! FUNCTION: Catalyzes the cleavage of the glycosidic bond of 2'.
deoxyribonucleosides and the transfer of the deoxyribosyl moiety
to an acceptor purine or pyrimidine base.
-! CATALYIT: 2-deoxy-D-ribosyl-base(1) + base(2) = 2-deoxy-D-ribosyl-base(1) + base(1).
-! BIOPHYSICOCHEMICAL PROPERTIES:
pH dependence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family.
-!- CAUTION: Was originally (Ref.1) thought to originate from E.coli.
                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE, PROTEIN SEQUENCE OF 1-25, FUNCTION, ACTIVE SITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: Nucleotide metabolism.
-!- SUBUNIT: Homohexamer.
-!- SIMILARITY: Belongs to the nucleoside deoxyribosyltransferase
                                                                                                                                                                                                                                                                                                        AND MUTAGENESIS OF GLU-97.
MEDLINE=95318137; PubMed=7797550; DOI=10.1074/jbc.270.26.15551;
Porter D.O.T., Merrill B.M., Short S.A.,
"Identification of the active site nucleophile in nucleoside 2-deoxyribosyltransferase as glutamic acid 98.";
J. Biol. Chem. 270:15551-15556(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB; 1F8X; X-ray; A/B=1-156.
PDB; 1F8Y; X-ray; A/B=1-156.
Interpro; 1FR007710; N_deoxyrib_trans.
Pfam; PP05014; Nuc_deoxyrib_tr; 1.
3D-structure; Direct protein sequencing; Nucleotide metabolism;
                                                                                                                                                                                         Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBI_TaxID=28039;
                                                                                                                                 ż
                                                                       25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
01.FBB-2005 (Rel. 46, Last annotation update)
Nucleoside deoxyribosyltransferase (EC 2.4.2.6)
                                     156 AA.
                                                                                                                                                       deoxyribosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Optimum pH is 6.0;
                                     STANDARD;
                                   NTD LACLE
Q9R5V5;
RESULT 1
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LACJO
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NTD_LACJO
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                                                                                                                                                                                                                                                                                                                                                                 64 EWASATYHNDLVGIKTSDVMLGVXLPEEEDVGLGMELGYALSQGKYILLVIPDEDYGKPI 123
                                                                                                                                                                                                                                                                                                                                        62 KVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 VWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPI 122
                                                                                                                                                                                                                                                                      1 PKKTIYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHD 60
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"Functional cloning, heterologous expression, and purification of two
different N-deoxyribosyltransferases from Lactobacillus helveticus.";
J. Biol. Chem. 277:14400-14407(2002).
BMBL, AY064167, AAL73114.1; -; Genomic_DNA.
HSSP, Q9RSV5; 1F8V.
SMR; Q8RLY4; 4-158.
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                                                                     E->A: Loss of transferase activity 3A3AEC3FD5B4743B CRC64;
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                                                                                                                                               Score 843; DB 1; Length 156;
Pred. No. 4.6e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 158;
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82.6%; Pred. No. 3.1e-54;
ive 20; Mismatches 7; Indels
                                                                                                                                                                                           0; Indels
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Lactobacillus.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 INLMSWGVSDNVIKMSQLKDFNFNKPRFDFYBGAVY 156
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InterPro; IPR007710; N deoxyrib_trans.
Pfam; PF05014; Nuc_deoxyrib_tr; 1.
                                                                                                                                                         100.0%; Prec. ...
                                              Nucleophile.
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97 Nu
97 E-
17949 MW;
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QBRLY4;
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QSFWM8 LACAC
ID QSFWM8_LACAC PRELIMINARY;
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                                                                                             156 AA;
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Best Local Similarity
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Transferase.
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                      INIT MET
ACT SITE
MUTAGEN
                                                                                             SEQUENCE
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                                                                                                                                               Query Match
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159 AA

PRT;

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66 WASATYHNDLIGIKSSDIMLGVYLPREEDVGLGMELGYALSQCKYILLVIPDEDYGKPIN 125
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PubMed-1988040; DOI=10.1073/pnas.0307327101;
Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,
Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
"The genome sequence of the probictic intestinal bacterium
Lactobacillus johnsonii NCC 533.";
Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
-I- FUNCTION: Catalyzes the cleavage of the glycosidic bond of 2'-
deoxyribonucleosides and the transfer of the deoxyribosyl moiety
to an acceptor purine or pyrimidine base (By similarity).
-I- CATALYTIC ACTIVITY: 2-deoxyr-base(1) + base(2) = 2-deoxyr-
D-ribosyl-base(2) + base(1).
                                                                                                                                                                                                                                                                                                             PubMed=15671160; DOI=10.1073/pnas.0409188102;
Altermann E., Russell W.M., Azcarate-Peril M.A., Barrangou R.,
Buck B.L., McAuliffe O., Souther N., Dobson A., Duong T., Callanan M.,
Lick S., Hamrick A., Cano R., Klaenhammer T.R.;
"Complete genome sequence of the probiotic lactic acid bacterium
Lactobacillus acidophilus NCFM.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 KTLYFGAGWFNEKQNKAYKAAMEALKQNPTVDLENSYVPLENQYKDIRVDEHPEYLHDIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 159;
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                                                                           2-deoxyribosyltransferase.
OrderedLocusNames=LBA0145;
Lactobacillus acidophilus.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.8%; Score 719; DB 2; L. 83.1%; Pred. No. 1.8e-53; ive 18; Mismatches 8;
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25-0CT-2004 (Rel. 45, Last sequence update)
13-5EP-2005 (Rel. 48, Last annotation update)
Nucleoside deoxyribosyltransferase (EC 2.4.2.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 LMSWGVCDNAIKISELKDFDFNKPRFNFYDGAVY 159
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Name=ntd; OrderedLocusNames=LJ0124;
Lactobacillus johnsonii.
10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
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                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
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Best Local Similarity
Matches 128; Conserv
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VWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPI 122
                                                                                                                                                                                                                                                                                                  [GENOMIC DNA]
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QBRLYS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Conservative
                                                                                                                                                                                                                                                                                                                                                     deoxyribosyltransferase."
Submitted (NOV-2001) to t
                                                                                                                                                                                                             deoxyribosyltransferase).
                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                      Lactobacillus fermentum.
                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
STRAIN=CIP 102980T;
Kaminski P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                         NCBI_TaxID=1613;
                                                                                                                                    NTD LACFE
Q6YNI5;
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                                                                                                              RESULT 6
NTD_LACFE
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                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                             NNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPINLMSWGV 129
                                                                                                                                                                                                                                                                                                                                         KKTIYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDK 62
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                                                                                                                                                                                                                                                    Gaps
 PATHWAY: Nucleotide metabolism.
SIMILARITY: Belongs to the nucleoside deoxyribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and expression of the nucleoside deoxyribosyltransferase-II gene from Lactobacillus helveticus."; Biosci. Biotechnol. Biochem. 64:2243-2245 (2000).
EMBL, AB039914; BAA92683.2; -; Genomic_DNA. PIR; JC7522; JC7522.
HSSP; QSR5V5; IFRY.
SNR; QSR5V5; 1FRY.
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MEDLINE=21012342; PubMed=11129605; DOI=10.1271/bbb.64.2243;
                                                                                                                                                                                                                            Length 149;
                                                                                                                                                                                                                                                   15; Indels
                                                                                                                                                 InterPro; IPR007710; N_deoxyrib_trans.

Pfam; PF05014; Nuc_deoxyrib_tr; 1.

Complete proteome; Nucleotide metabolism; Transferase.

ACT_SITE

SEQUENCE 149 AA; 16941 MW; 6CB8A86B0553152A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Firmicutes, Lactobacillales, Lactobacillaceae, Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 AA; 18318 MW; D661273AD89309CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Nucleoside deoxyribosyltransferase-II.
                                                                                                                                                                                                                          77.0%; Score 653; DB 1;
80.4%; Pred. No. 7.3e-48;
iive 14; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016740; F:transferase activity; IEA
                                                                                                                           EMBL; AE017200; AAS08106.1; -; Genomic_DNA.
SMR; Q74LQ9; 2-149.
                                                                                                                                                                                                                                                                                                                                                                                           SDNVIKMSQLKDFNFNKPRFDFYEGAVY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007710; N_deoxyrib_trans
Pfam; PF05014; Nuc_deoxyrib_tr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEKWPO LACHE PRELIMINARY;
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactobacillus helveticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okuyama K., Noguchi T.;
                                                                                                                                                                                                                                        Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1587;
                                                                                                                                                                                                                                                                                                                             20
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                                                                                                                                                                                                                             Query Match
                                                                                                      removed.
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 QIATYNNDLNAVGTSDVCVALYDMDQIDEGICMEIGMFVALHKPIVLLPFTKKDKSAYEA 129
64 BWASATYHNDLYGIKTSDVLLGVYLPQEEHVGLGMELGYPLSQGKLFFWFSHMKDYGKPI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

FUNCTION: Catalyzes the cleavage of the glycosidic bond of 2'-
deoxyribonucleosides and the transfer of the deoxyribosyl moiety
to an acceptor purine or pyrimidine base (By similarity).

CATALYTIC ACTIVITY: 2-deoxy-D-ribosyl-base(1) + base(2) = 2-deoxy-
D-ribosyl-base(2) + base(1).

PATHWAY: Nucleotide metabolism.
SIMILARITY: Belongs to the nucleoside deoxyribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 IYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDKV-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 IYLATSFFNEEQRARIPQALAQLEANPTVGVVHQ--PFDFQYKDARVDSDPAGVFGSLEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 103 Nucleophile (By similarity).
168 AA; 18896 MW; 362162F43586C317 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characteriztion of the Lactobacillus fermentum N-
                                                                                                                                    25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Nucleoside deoxyribosyltransferase (EC 2.4.2.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Æ
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                                                                                                123 NLMSWGVSDNVIKMSQLKDFNFNKPRFDFYEGAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AY064168, AAL73115.1; -; Genomic_DNA.
InterPro; IPR007710; N_deoxyrib_trans.
Pfam; PF05014; Nuc deoxyrib_tr; 1.
Nucleotide metabollism; Transferase.
ACT SITE 103 103
SEQÜENCE 168 AA; 18896 MW; 362162F43586
                                                                                                                                                                                                                                                                                                                                             168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167
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NCBI_TaxID=1360;
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       'Complete
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OKUYAMA K., NOGUCHI T.;

OKUYAMA K., NOGUCHI T.;

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

B. Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

B. BMBL; AB076365; AAL73113.1; -; Genomic_DNA.

B. BMBJ; AB076365; BA00952.1; -; Genomic_DNA.

R. BDB; 182D; X-ray; A/B/C=1-167.

R. PDB; 182L; X-ray; A/B/C=1-167.

R. PDB; 183F; X-ray; A/B/C=1-167.

R. PDB; 183F; X-ray; A/B/C=1-167.

R. GO; GO:005044; F:uclosside decoxyribosyltransferase activity; IEA.

GO; GO:0016757; F:transferase activity, transferring glycosyl. ..; IEA

InterPor, IRRO/7710; M. decoxyrib_trans.

R. Pam; PF05014; Nuc decoxyrib_trans.

R. Pam; PF05014; Nuc decoxyrib_trans.

R. Pam; PF05014; Nuc decoxyrib_trans.
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PubMed=15671160; DOI=10.1073/pnas.0409188102;
Altermann E., Russell W.M., Azcarate-Peril M.A., Barrangou R.,
Buck B.L., McAuliffe O., Souther N., Dobson A., Duong T., Callanan M.,
Lick S., Hamrick A., Cano R., Klaenhammer T.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MPKKTIYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional cloning, heterologous expression, and purification of two different N-deoxyribosyltransferases from Lactobacillus helveticus."; J. Biol. Chem. 277:14400-14407(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
01-JUN-2002 (TrEMBLrel. 21, Created)
1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Purine trans deoxyribosylase (Nucleoside deoxyribosyltransferase-I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CNRZ32;
MEDLINE=21964041; PubMed=11836245; DOI=10.1074/jbc.M111995200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.2%; Score 171.5; DB 2; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactobacillus acidophilus.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                  Name=ptd; Synonyms=ndtA;
Lactobacillus helveticus.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 AA; 18713 MW; 5540581511CB4787 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::: | :||| : ||: || EEE--KKMILMIAQGVTTIIDGNTEFEKLADYNFNE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 1.1e-06; 34; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSFINO LACAC PRELIMINARY;
QSFINO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 31.4
1es 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaminski P.A.;
                                                                                                                                                                                                                                                                 Lactobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis ILA403.";
Genome Res. 11:731-753(2001).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein yejD.
Name-yejD; OrderedLocusNames=LL0493;
Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaee; Lactococcus.
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acid bacterium
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                     Lactobacillus acidophilus NCFM.";
Proc. Natl. Acad. Sci. U.S.A. 102:3906-3912 (2005).
EMBL; CP000033; AAV43444.1; -; Genomic_DNA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR007710; N_deoxyrib_trans.
FPGM, FPGSO4; Nuc_deoxyrib_tr; 1.
Complete proteome; Transferase.
SEQUENCE 167 AA; 18933 WW; A80408F06C3E4D98 CRC64;
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InterPro; IPR007710; N deoxyrib_trans.
Pfam; PF05014; Nuc_deoxyrib_tr; 1.
Complete protecome: Hypothetical protein.
SEQUENCE 159 AA; 18295 MW; 98EAE589D9C099C3 CRC64;
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genome sequence of the probiotic lactic
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18.2%; Score 154.5; DB 2;
Best Local Similarity 32.5%; Pred. No. 3e-05;
Matches 49; Conservative 25; Mismatches 60;
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Q9CI73;
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155 AA; 16887 MW; A9C053404F8D13F0 CRC64;
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01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 IYPGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDKVWA 65
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Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

EMBL; CT005262; CAJ05145.1; -; Genomic_DNA.
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Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22480296; PubMed=1256656; DOI=10.1073/pnas.0337704100; Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D., Kleerebezem M., Eder R., Tarchini R., Peters S.A., Sandbrink H.M., Fiers M.W.B.J., Stiekema W., Klein Lankhorst R.M., Bron P.A., Hoffer S.M., Nierop Groof M.N., Kerkhoven R., De Vries M., Ursing De Vos W.M., Siezen R.J.;
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Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).

EMBL; AL935262; CAD65499.1; -; Genomic_DNA.
InterPro; IPR007710; N_deoxyrib_trans.
Pfam, PF05014; Nuc_deoxyrib_tril.
Complete proteome; Hypothetical protein.
SEQUENCE 157 AA; 17604 MW; 1581FB138FE1F6746 CRC64;
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24.6%; Pred. No. 0.01;
:ive 30; Mismatches 50; Indels
                                                                                    01-JUN-2003 (TTEMBLrel. 24, Last sequence update)
01-OCT-2003 (TTEMBLrel. 25, Last annotation update)
Hypothetical protein lp 3397.
OrderedLocusNames=lp 3397;
Lactobacillus plantarum.
Bacteria; Firmicutes; Lactobacillase; Lactobacillus.
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                                                                         01-JUN-2003 (TrEMBLrel. 24,
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QQQXO LEIMA PRELIMINARY;
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Matches 31; Conservative
                       Q88SL4_LACPL PRELIMINARY;
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ORFNames=LmjF23.1580;
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Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
Fiters M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Niezep Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
De Vos W.M., Siezen R.J.,
"Complete genome sequence of Lactobacillus plantarum WCFS1.";
Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).
EMBL, AL935256; CAB63892.1; -; Genomic_DNA.
InterPro; IRR007710; N deoxyrib_trans.
Pfam; PP05014; Nuc_deoxyrib_trans.
Complete protecome; Hypothetical protein.
SEQUENCE 146 AA; 16608 MW; E33D94B52F7BEZA9 CRC64;
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                                                                                                       4 KTIYF-GAGWFTDRQNKAYKEAMEA-LKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHD
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                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Gaps
                                                           42;
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          Length 155;
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                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactobacillus plantarum.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein 1p 1427.
OrderedLousNames=1p 1427;
                                                           47;
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       12.5%; Score 106; DB 2; 27.6%; Pred. No. 0.39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 LM----SWGVSDNVIKMSQLKDFNFNK-PRFDF 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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ative 28; Mismatches
                                                           16; Mismatches
                                                                                                                                                                                                                                                                                                        ----- 125
                                                                                                                                                                                                                                                                                                                                                      106 MVEKYGGEMAEGLSVENFGLPFNLM 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Query Match
Best Local Similarity 27.6%
Matches 40; Conservative
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Q9EMRO;
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Job time : 238 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : :: | | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | : : | | : : | : | : : | | : : | : : | : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : | : : | : : | : : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- GKYVLLV-IPDEDYG-----KPINLMSWGVSDNVIKMSQLKDFNFNKPRFDFY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTD--RQNKAYKEAMEALKENPTIDLEN-----SYVPLD-----NQYKGIRVDEH
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                   Amsacta moorei entomopoxvirus (AmEPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
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STRAIN=CB: TISSUE=Bursa;
Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
Full-length cDNAs from chicken bursal lymphocytes to facilitate
genefunction analysis.,
Genome Biol. 6:R6-R6(2005).
GO: GO:0005524; F:ATP-binding; IEA.
GO: GO:0008026; F:ATP-binding; IEA.
GO: GO:0003676; F:RICleic acid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                        "Complete genomic sequence of the Amsacta moorei entomopoxvirus: analysis and comparison with other poxviruses."; virology 274:120-139(2000).
EMBL; AF2502849; ARGO2845.1; -; Genomic DNA.
SEQUENCE 1149 AA; 135479 MW; 7E4EE54A13F87691 CRC64;
                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
MEDLINE=20396580; PubMed=10936094; DOI=10.1006/viro.2000.0449;
                                                                                                                                                                                                                                                                                                        Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W., Moyer R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 96; DB 2; Length 1149; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62; Indels
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SEQUENCE 1029 AA; 116048 MW; EC8909BE178AF562 CRC64;
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InterPro; IPR011545; DEAD/DEAH.N.
InterPro; IPR012651; DSHCT.
InterPro; IPR012650; Helicase_C.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; Helicase_C; SMART; SM00487; DEXDC; I.
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Best Local Similarity 23...
Best Local Conservative
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QSZMQ1;
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ORFNames=RCJMB04 1h14
                                                                                                                                       Betaentomopoxvirus.
NCBI_TaxID=28321;
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                                   Name=AMV139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 T----NDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPINLMSWGVSDN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 TIQKYGNNI---GFLKDER-----RLNVALTRAKDSLWIIGDK-----TNLQKNSTWDS 136
                                                                                           1 MPKKTIYF-----KENPTID-- 35
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                                                                                                                                      478 MPARTVLFTSASKFDGKDFRWISSGEYIQMSGRAGRRGMDDRGIVILMVDEKMSPTIGKQ
                                                                                                                                                                                      36 -LENSYVPLDNQY-----KGIRVDE-HPEYLHDKVWATATYNNDLNGI-----KTND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 KAYKBAMEALKENPTIDLENSYVPLDNQYKGIR-VDEHPEYLHDKVWATATYNNDLNGIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 11.0%; Score 93.5; DB 2; Length 264; Local Similarity 27.1%; Pred. No. 8.3; les 39; Conservative 24; Mismatches 52; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
  Length 1029;
                                               56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 264 264 264 264 AA; 31399 MW; EDD7A47344723240 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
ORFNames=PB000574.01.0;
Query Match 11.2%; Score 95; DB 2; Best Local Similarity 22.4%; Pred. No. 29; Matches 45; Conservative 32; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary data.
EMBL; CAAI01001273; CAH96134.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 AA
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                                                                                                                                                                                                                                                                                                                                                                          120 KPINLMSWGVSDNVIKMSQLK 140
                                                                                                                                                                                                                                                                                                                                                                                                                     ------WGVVVNFSKKSNVK 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q4Z0Q6_PLABE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein
NON TER 264 26
SEQUENCE 264 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium berghei
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